

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2005, 21:17:08 ; Search time 153.792 Seconds
(without alignments)
791.381 Million cell updates/sec

Title: US-10-029-926D-25

Perfect score: 1440

Sequence: 1 MKYLLPTAAGALLLAQA.....VLGAARQLISEEDLNGAA 277

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21.*

1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1440	100.0	277	5	ABG78150 Human Fv
2	1440	100.0	277	5	ABG91841 Human ant
3	1436	99.7	277	8	ADI28366 Human scf
4	1436	99.7	277	8	AD882026 Human pla
5	1416	98.3	277	5	ABG78328 Human Fv
6	1416	98.3	277	5	ABG92019 Human ant
7	1397.5	97.0	278	8	ADI28367 Human scf
8	1397.5	97.0	278	8	AD882027 Human pla
9	1393.5	96.8	280	8	ADI57363 P-selecti
10	1393.5	96.8	280	8	ADT63078 Human scf
11	1388.5	96.4	280	9	ADX01131 Amino aci
12	1388.5	96.4	280	9	ADY78325 Single ch
13	1386.5	96.3	280	8	ADI28368 Human scf
14	1386.5	96.3	280	8	AD882028 Human leu
15	1379.5	95.8	280	9	ADX01181 Amino aci
16	1379.5	95.8	280	9	ADX01130 Amino aci
17	1379.5	95.8	280	9	ADY78324 Single ch
18	1379.5	95.8	280	9	ADY78375 Single ch
19	1378.5	95.7	280	9	ADX01185 Amino aci
20	1378.5	95.7	280	9	ADY78379 Single ch
21	1378	95.7	265	5	ABG92020 Human ant
22	1375.5	95.5	280	9	ADX01186 Amino aci
23	1375.5	95.5	280	9	ADY78380 Single ch
24	1374.5	95.5	280	9	ADX01180 Amino aci

25	1374.5	95.5	280	9	ADY78374
26	1294	89.9	291	8	ADN06989
27	1278.5	88.8	282	4	AAE02185
28	1275.5	88.6	309	2	AAW83322
29	1275.5	88.6	309	5	ABB09603
30	1275.5	88.6	309	6	ABG74384
31	1275.5	88.6	309	7	ADG98737
32	1275.5	88.6	309	8	ADO40446
33	1257	87.3	246	5	ABG78329
34	1257	87.3	246	5	ABG92026
35	1250	86.8	256	5	ABG78334
36	1250	86.8	256	5	ABG92025
37	1240	86.1	244	9	ADW90315
38	1240	86.1	244	9	ADX01815
39	1231.5	85.5	260	5	ABG92023
40	1223	84.9	263	5	ABG92024
41	1218.5	84.6	239	5	ABP44926
42	1218.5	84.6	239	7	ADG95753
43	1212.5	84.2	239	5	ABP46027
44	1212.5	84.2	239	7	ADG96854
45	1201.5	83.4	290	6	ABP55318

ALIGNMENTS

RESULT 1

ABG78150
ID ABG78150 standard; protein; 277 AA.

XX AC ABG78150;

DT 15-NOV-2002 (first entry)

DE Human Fv molecule hypervariable region related peptide #25.

XX Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.

XX Homo sapiens.

OS WO200259264-A2.

XX 01-AUG-2002.

PF 31-DEC-2001; 2001WO-US049440.

XX 29-DEC-2000; 2000US-00751181.

PR (BIOT-) BIO-TECHNOLOGY GEN CORP.

PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
Plaksin D, Peretz T;

DR WPI; 2002-619166/66.

XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
PT or fragment, or construct of fragment with enhanced binding
PT characteristics so as to selectively bind target cell in favor of other
cells.

PS Claim 4; Page 155-156; 232pp; English.

XX The invention relates to a peptide or polypeptide comprising an Fv
CC molecule, a construct or fragments or a construct of a fragment with
CC enhanced binding characteristics which selectively and/or specifically
CC binds to a target cell in favour of other cells, where binding is
CC primarily determined by a first hypervariable region and Fv is a single
CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
CC association with or attached, coupled, combined, linked or fused to a
CC pharmaceutical agent, is useful in the manufacture of a medicament, where
CC the medicament has activity against a diseased cell, preferably a cancer

CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
 CC acute myeloid leukemia cell). The peptide is also useful for preparing a
 CC composition for use in inhibiting the growth of a diseased or cancer
 CC cell. This sequence represents a human Fv molecule hypervariable region
 CC related peptide of the invention

XX Sequence 277 AA;

Query Match 100.0%; Score 1440; DB 5; Length 277;
 Best Local Similarity 100.0%; Pred. No. 5.2e-89;
 Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKYLLPTAAAGLLLLAAQAPMAAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDDYGMWVR 60
 DB 1 MKYLLPTAAAGLLLLAAQAPMAAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDDYGMWVR 60
 QY 61 QAPKGLEWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQMNSLRADTAIVYCAR 120
 DB 61 QAPKGLEWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQMNSLRADTAIVYCAR 120
 QY 121 MRAPVIWGQGLTVTVSRGG 180
 DB 121 MRAPVIWGQGLTVTVSRGG 180
 QY 181 YYASWYQQKPGQAPVLIYGNKRRPSGIPDRFGSSSGNTASITITGAQAEADADYYCNS 240
 DB 181 YYASWYQQKPGQAPVLIYGNKRRPSGIPDRFGSSSGNTASITITGAQAEADADYYCNS 240
 QY 241 RDSGNGHVFGGQTKLTVLGAABEQKLISEEDLNGAA 277
 DB 241 RDSGNGHVFGGQTKLTVLGAABEQKLISEEDLNGAA 277

RESULT 2

ABG91841
 ID ABG91841 standard; protein; 277 AA.
 XX
 AC ABG91841;
 XX
 DT 04-DEC-2002 (first entry)
 XX
 DE Human antibody fragment #25.
 XX
 KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
 KW metastasis; hypervariable region; autoimmune disease; thrombosis;
 KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
 KW myocardial infarction; retinopathic disease; abnormal platelet function;
 KW sulphated tyrosine-dependent protein-protein interaction.
 XX
 OS Homo sapiens.
 XX
 PN WO200253700-A2.
 XX
 PD 11-JUL-2002.
 XX
 XX 31-DEC-2001; 2001WO-US049442.
 XX
 XX 29-DEC-2000; 2000US-00751181.
 XX 29-DEC-2000; 2000US-0258948P.
 XX
 XX (BIOT-) BIO-TECHNOLOGY GEN CORP.
 XX
 XX Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
 XX Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
 XX WPI; 2002-674776/72.
 XX
 XX Novel isolated epitope present on cancer cells and important in
 XX physiological phenomena such as cell rolling, metastasis and
 XX inflammation, for treating autoimmune, inflammatory or cardiovascular
 XX diseases, and cancer.

PS Claim 23; Page 233-234; Opp; English.

XX The invention relates to an isolated epitope present on cancer cells and
 CC important in physiological phenomena such as cell rolling, metastasis and
 CC inflammation, where the epitope is capable of being bound by an antibody,
 CC its antigen-binding fragment or its complex comprising at least one
 CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia
 CC cells in a patient, or in the manufacture of a medicament for the above
 CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents a human antibody fragment
 CC of the invention

XX Sequence 277 AA;

Query Match 100.0%; Score 1440; DB 5; Length 277;
 Best Local Similarity 100.0%; Pred. No. 5.2e-89;
 Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKYLLPTAAAGLLLLAAQAPMAAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDDYGMWVR 60
 DB 1 MKYLLPTAAAGLLLLAAQAPMAAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDDYGMWVR 60
 QY 61 QAPKGLEWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQMNSLRADTAIVYCAR 120
 DB 61 QAPKGLEWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQMNSLRADTAIVYCAR 120
 QY 121 MRAPVIWGQGLTVTVSRGG 180
 DB 121 MRAPVIWGQGLTVTVSRGG 180
 QY 181 YYASWYQQKPGQAPVLIYGNKRRPSGIPDRFGSSSGNTASITITGAQAEADADYYCNS 240
 DB 181 YYASWYQQKPGQAPVLIYGNKRRPSGIPDRFGSSSGNTASITITGAQAEADADYYCNS 240
 QY 241 RDSGNGHVFGGQTKLTVLGAABEQKLISEEDLNGAA 277
 DB 241 RDSGNGHVFGGQTKLTVLGAABEQKLISEEDLNGAA 277

RESULT 3

AD128366
 ID AD128366 standard; protein; 277 AA.
 XX
 AC AD128366;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human scFv fragment Y1, binds to platelets.
 XX
 KW Human; antibody; scFv; platelet; drug delivery; cancer; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO2004002528-A1.
 XX
 XX 08-JAN-2004.
 XX
 XX 30-JUN-2003; 2003WO-US020604.
 XX
 XX 01-JUL-2002; 2002US-00189025.

(SAVI-) SAVIENT PHARM INC.

Lazarovits J, Nimrod A, Hoch-Mar-Chaim H, Levanon A;

WPI; 2004-099189/10.

Composition comprising an agent and/or antibody or its fragment, useful for treating auto-immune disease, thrombosis, restenosis, metastasis, or for inhibiting growth and/or replication of tumor cells or leukemia cells.

Claim 13; SEQ ID NO 1; 58pp; English.

The present sequence is the protein sequence of human scFv fragment Y1. This antibody was identified by screening a human antibody phage library that has diversity only in the heavy chain CDR3 regions. Fixed human platelets were screened in order to identify antibodies that bind platelets. The epitope for Y1 antibody is located between amino acids 272 and 285 on glyocalicin, a subunit of the CD42 complex. Y1 also binds the N-terminal of PSEL-1, a receptor for E-, L- and P-selectins, and has a high affinity for primary leukemia cells. The invention relates to compositions utilising an agent and an antibody or its fragment. The agent is a toxin, radioisotope or pharmaceutical agent such as doxorubicin. It is complexed or combined with or conjugated to the antibody or its fragment. The agent and/or antibody can be present in the composition is a sub-clinical amount, i.e. less than the amount generally found to be clinically effective when the agent is administered alone. The composition is used in claimed methods of: inhibiting cell rolling, inflammation, thrombosis, restenosis, metastasis, the growth and/or replication of tumor cells or leukemia cells, an increase in number of tumor or leukemia cells, cell-cell, cell-matrix, platelet-matrix, platelet-platelet and/or cell-platelet complex formation, aggregation or adhesion; increasing the mortality rate of tumor or leukemia cells, the susceptibility of disease cells to damage by anti-disease agents, and the susceptibility of tumor or leukemia cells to damage by anti-cancer agents; and ameliorating the effects of a disease, preventing a disease, treating a disease or inhibiting the progress of a disease.

Sequence 277 AA;

Query Match 99.7%; Score 1436; DB 8; Length 277;

Best Local Similarity 99.6%; Pred. No. 9.6e-89;

Matches 276; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKYLLPTAAAGLLLLAAQPMARVQLVSGGGVVRPGGSLRLSCAASGFTDDYGMWVR 60

DB 1 MKYLLPTAAAGLLLLAAQPMARVQLVSGGGVVRPGGSLRLSCAASGFTDDYGMWVR 60

QY 61 QAPGKGLWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCAR 120

DB 61 QAPGKGLWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCAR 120

QY 121 MRAPVINGQGLTVTVSRGGGGGGGGGGSSSELTDQPAVSVALGQTVRITCGDSLRS 180

DB 121 MRAPVINGQGLTVTVSRGGGGGGGGGGSSSELTDQPAVSVALGQTVRITCGDSLRS 180

QY 181 YYASWYQKPGQAPVLIYGNKRRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNS 240

DB 181 YYASWYQKPGQAPVLIYGNKRRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNS 240

QY 241 RDSGNGHVFVGGGFKLVLAAGAAEQKLI SEEDLNGAA 277

DB 241 RDSGNGHVFVGGGFKLVLAAGAAEQKLI SEEDLNGAA 277

RESULT 4

ADS82026

ID ADS82026 standard; protein; 277 AA.

AC ADS82026;

XX 30-DEC-2004 (first entry)

DT 30-DEC-2004 (first entry)

XX

Human platelet binding scFv antibody fragment Y1.

cell rolling; inflammation; autoimmunity disease; thrombosis; restenosis; metastasis; tumour; leukaemia; cardiovascular disease; retinopathy; human; scFv; antibody; cytostatic; antiinflammatory; thrombolytic; vasotropic; immunosuppressive; cardiovascular-Gen; ophthalmological.

Homo sapiens.

US2004202665-A1.

14-OCT-2004.

30-JUN-2003; 2003US-00610843.

01-JUL-2002; 2002US-0393453P.

(LAZA/) LAZAROVITS J.

(NIMR/) NIMROD A.

(HOCH/) HOCH M H.

(LEVA/) LEVANON A.

Lazarovits J, Nimrod A, Hoch MH, Levanon A;

WPI; 2004-746943/73.

Composition useful for treating diseases e.g., inflammatory diseases, thrombosis, restenosis, autoimmunity diseases, cardiovascular diseases or retinopathic diseases, comprises agent and antibody or its fragment.

Claim 13; SEQ ID NO 1; 22pp; English.

The invention relates to a composition which comprises an agent and an antibody or its fragment. The composition is useful for inhibiting cell rolling, inflammation, autoimmunity disease, thrombosis, restenosis, metastasis, cell-cell, cell-matrix, platelet-matrix, platelet-platelet and/or cell-platelet complex formation, aggregation or adhesion, increase in number of tumor cells or growth and/or replication of tumor or leukemia cells, for increasing the mortality rate of tumor or leukemia cells, the susceptibility of tumor or leukemia cells to damage by anti-cancer agents, for decreasing number of tumor or leukemia cells, or for ameliorating the effect of a disease, preventing a disease, treating a disease, or inhibiting the progress of a disease. The composition is useful for therapeutic treatment, where antibody or its fragment and the agent are administered separately. The antibody or its fragment is administered prior to or subsequent to the agent. The composition is useful for treating diseases such as inflammatory diseases, diseases involving abnormal or pathogenic adhesion, thrombosis and/or restenosis, diseases involving abnormal or pathogenic aggregation, autoimmunity diseases, cardiovascular diseases, retinopathic diseases, diseases caused by sulphated tyrosine-dependent protein-protein interactions or diseased cells. The present sequence represents the human platelet binding scFv antibody fragment Y1.

Sequence 277 AA;

Query Match 99.7%; Score 1436; DB 8; Length 277;

Best Local Similarity 99.6%; Pred. No. 9.6e-89;

Matches 276; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKYLLPTAAAGLLLLAAQPMARVQLVSGGGVVRPGGSLRLSCAASGFTDDYGMWVR 60

DB 1 MKYLLPTAAAGLLLLAAQPMARVQLVSGGGVVRPGGSLRLSCAASGFTDDYGMWVR 60

QY 61 QAPGKGLWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCAR 120

DB 61 QAPGKGLWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCAR 120

QY 121 MRAPVINGQGLTVTVSRGGGGGGGGGGSSSELTDQPAVSVALGQTVRITCGDSLRS 180

DB 121 MRAPVINGQGLTVTVSRGGGGGGGGGGSSSELTDQPAVSVALGQTVRITCGDSLRS 180

QY 181 YYASWYQKPGQAPVLIYGNKRRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNS 240

CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents a human antibody fragment
 CC of the invention
 XX
 SQ Sequence 277 AA;
 Query Match 98.3%; Score 1416; DB 5; Length 277;
 Best Local Similarity 98.2%; Pred. No. 2.1e-87;
 Matches 272; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 MKYLLPTAAAGLLLLAAQPAEAQVQLVSGGVRPGGSLRLSCAASGFTFDYDGMSSWR 60
 Db 1 MKYLLPTAAAGLLLLAAQPAEAQVQLVSGGVRPGGSLRLSCAASGFTFDYDGMSSWR 60
 Qy 61 QAPKGLEWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCAR 120
 Db 61 QAPKGLEWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCAR 120
 Qy 121 MRAPVWGQGLTVTVSRGGSGGGSGGSSSLTQDPAVSVAGTQVTRITCGDSLRS 180
 Db 121 LTHPYFGQGLTVTVSRGGSGGGSGGSSSLTQDPAVSVAGTQVTRITCGDSLRS 180
 Qy 181 YYASWYQKPGQAPVLIYGNKRPSPGIPDRFGSSSGNTASLTITGAQAEDEADYYCNS 240
 Db 181 YYASWYQKPGQAPVLIYGNKRPSPGIPDRFGSSSGNTASLTITGAQAEDEADYYCNS 240
 Qy 241 RDSGSGNHVFGGTKTLVLGAAAEQKLISEEDLNGAA 277
 Db 241 RDSGSGNHVFGGTKTLVLGAAAEQKLISEEDLNGAA 277
 RESULT 7
 ADI28367
 ID ADI28367 standard; protein; 278 AA.
 XX
 AC ADI28367;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human scFv fragment Y17, binds to platelets.
 XX
 KW Human; antibody; scFv; platelet; drug delivery; cancer; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO2004002528-A1.
 XX
 PD 08-JAN-2004.
 XX
 PF 30-JUN-2003; 2003WO-US020604.
 XX
 PR 01-JUL-2002; 2002US-00189025.
 XX
 PA (SAVI-) SAVIENT PHARM INC.
 XX
 PI Lazarovits J, Nimrod A, Hoch-Mar-Chaim H, Levanon A;
 XX
 DR WPI; 2004-099189/10.
 XX
 PT Composition comprising an agent and/or antibody or its fragment, useful
 PT for treating auto-immune disease, thrombosis, restenosis, metastasis, or
 PT for inhibiting growth and/or replication of tumor cells or leukemia
 PT cells.
 XX
 PS Claim 13; SEQ ID NO 2; 58pp; English.
 XX
 PS The present sequence is the protein sequence of human scFv fragment Y17.
 CC This antibody was identified by screening a human antibody phage library
 CC that has diversity only in the heavy chain CDR3 regions. Fixed human
 CC platelets were screened in order to identify antibodies that bind

CC platelets. Y17 binds leukaemic cells. The invention relates to
 CC compositions utilising an agent and an antibody or its fragment. The
 CC agent is a toxin, radioisotope or pharmaceutical agent such as
 CC doxorubicin. It is complexed or combined with or conjugated to the
 CC antibody or its fragment. The agent and/or antibody can be present in the
 CC composition is a sub-clinical amount, i.e. less than the amount generally
 CC found to be clinically effective when the agent is administered alone.
 CC The composition is used in claimed methods of: inhibiting cell rolling,
 CC inflammation, thrombosis, restenosis, metastasis, the growth and/or
 CC replication of tumour cells or leukaemia cells, an increase in number of
 CC tumour or leukaemia cells, cell-cell, cell-matrix, platelet-matrix,
 CC platelet-platelet and/or cell-platelet complex formation, aggregation or
 CC adhesion; increasing the mortality rate of tumour or leukaemia cells, the
 CC susceptibility of disease cells to damage by anti-disease agents, and the
 CC susceptibility of tumour or leukaemia cells to damage by anti-cancer
 CC agents; and ameliorating the effects of a disease, preventing a disease,
 CC treating a disease or inhibiting the progress of a disease.
 XX
 SQ Sequence 278 AA;
 Query Match 97.0%; Score 1397.5; DB 8; Length 278;
 Best Local Similarity 97.8%; Pred. No. 3.8e-86;
 Matches 272; Conservative 1; Mismatches 4; Indels 1; Gaps 1;
 Qy 1 MKYLLPTAAAGLLLLAAQPAEAQVQLVSGGVRPGGSLRLSCAASGFTFDYDGMSSW 59
 Db 1 MKYLLPTAAAGLLLLAAQPAEAQVQLVSGGVRPGGSLRLSCAASGFTFDLTHPYFW 60
 Qy 60 RQAPKGLEWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCA 119
 Db 61 RQAPKGLEWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCA 120
 Qy 120 RMRAPVWGQGLTVTVSRGGSGGGSGGSSSLTQDPAVSVAGTQVTRITCGDSLRL 179
 Db 121 RMRAPVWGQGLTVTVSRGGSGGGSGGSSSLTQDPAVSVAGTQVTRITCGDSLRL 180
 Qy 180 SYTASWYQKPGQAPVLIYGNKRPSPGIPDRFGSSSGNTASLTITGAQAEDEADYYC 239
 Db 181 SYTASWYQKPGQAPVLIYGNKRPSPGIPDRFGSSSGNTASLTITGAQAEDEADYYC 240
 Qy 240 SRDSSGNGHVFGGTKTLVLGAAAEQKLISEEDLNGAA 277
 Db 241 SRDSSGNGHVFGGTKTLVLGAAAEQKLISEEDLNGAA 278
 RESULT 8
 ADS82027
 ID ADS82027 standard; protein; 278 AA.
 XX
 AC ADS82027;
 XX
 DT 30-DEC-2004 (first entry)
 XX
 DE Human platelet binding scFv antibody fragment Y17.
 XX
 KW cell rolling; inflammation; autoimmune disease; thrombosis; restenosis;
 KW metastasis; tumour; leukaemia; cardiovascular disease; retinopathy;
 KW human; scFv; antibody; cytostatic; antiinflammatory; thrombolytic;
 KW vasotropic; immunosuppressive; cardiovascular-Gen; ophthalmological.
 XX
 OS Homo sapiens.
 XX
 PN US2004202665-A1.
 XX
 PD 14-OCT-2004.
 XX
 PF 30-JUN-2003; 2003US-00610843.
 XX
 PR 01-JUL-2002; 2002US-0393453P.
 XX
 PA (LAZA/) LAZAROVITS J.
 XX (NIMR/) NIMROD A.
 PA (HOCH/) HOCH M H.

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PA (LEVA/) LEVANON A.
XX
XX
PI Lazarovits J, Nimrod A, Hoch MH, Levanon A;
XX
XX WPI; 2004-746943/73.
XX
XX Composition useful for treating diseases e.g., inflammatory diseases,
XX thrombosis, restenosis, autoimmune diseases, cardiovascular diseases or
XX retinopathic diseases, comprises agent and antibody or its fragment.
XX
XX Claim 13; SEQ ID NO 2; 22pp; English.
XX
XX The invention relates to a composition which comprises an agent and an
XX antibody of its fragment. The composition is useful for inhibiting cell
XX rolling, inflammation, autoimmune disease, thrombosis, restenosis,
XX metastasis, cell-cell, cell-matrix, platelet-matrix, platelet-platelet
XX and/or cell-platelet complex formation, aggregation or adhesion, increase
XX in number of tumour cells or growth and/or replication of tumour or
XX leukaemia cells, for increasing the mortality rate of tumour or leukaemia
XX cells, the susceptibility of tumour or leukaemia cells to damage by anti-
XX cancer agents, for decreasing number of tumour or leukaemia cells, or for
XX ameliorating the effect of a disease, preventing a disease, treating a
XX disease, or inhibiting the progress of a disease. The composition is
XX useful for therapeutic treatment, where antibody or its fragment and the
XX agent are administered separately. The antibody or its fragment is
XX administered prior to or subsequent to the agent. The composition is
XX useful for treating diseases such as inflammatory diseases, diseases
XX involving abnormal or pathogenic adhesion, thrombosis and/or restenosis,
XX diseases involving abnormal or pathogenic aggregation, autoimmune
XX diseases, cardiovascular diseases, retinopathic diseases, diseases caused
XX by sulphated tyrosine-dependent protein-protein interactions or diseased
XX cells. The present sequence represents the human platelet binding scfv
XX antibody fragment Y17.
XX
XX Sequence 278 AA;
XX
XX Query Match 97.0%; Score 1397.5; DB 8; Length 278;
XX Best Local Similarity 97.8%; Pred. No. 3.8e-85; Mismatches 1; Indels 1; Gaps 1;
XX Matches 272; Conservative 1; Mismatches 4; Indels 1; Gaps 1;
QY 1 MKYLLPTAAAGLLLLAAQPAEAQVQLVSGGQVVRPGGSLRLSCAASGFTFD-DYGM5W 59
Db 1 MKYLLPTAAAGLLLLAAQPAEAQVQLVSGGQVVRPGGSLRLSCAASGFTFDLTHPFW 60
QY 60 RQAPGKLEWVSGINWNGSTGYADSVKGRFTISRDNAKNSLYLQMSLRAEDTAVYCA 119
Db 61 RQAPGKLEWVSGINWNGSTGYADSVKGRFTISRDNAKNSLYLQMSLRAEDTAVYCA 120
QY 120 RMRAPVWGQGLTVTSRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 179
Db 121 RMRAPVWGQGLTVTSRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 180
QY 180 SYVASWYQQKPGAPQAPLVLYYKNNRPSGIPDRFSGSSSGNTASITITGAQAEADYYCN 239
Db 181 SYVASWYQQKPGAPQAPLVLYYKNNRPSGIPDRFSGSSSGNTASITITGAQAEADYYCN 240
QY 240 SRDSSGNHVVFGGQTKLVTLGAABEQKLISEEDINGAA 277
Db 241 SRDSSGNHVVFGGQTKLVTLGAABEQKLISEEDINGAA 278
RESULT 9
ADJ57363
ID ADJ57363 standard; protein; 280 AA.
XX
XX AC ADJ57363;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE P-selectin glycoprotein ligand-1-binding scFv antibody fragment I32.
XX
XX KW P-selectin glycoprotein ligand-1; PSGL-1; antibody; scFv; cytostatic;
XX antiinflammatory; immunosuppressive; human.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX Region 53..60
XX /label= CDR1
XX /note= "Specifically referred to in Claim 2"
XX
XX FT 75..90
XX /label= CDR2
XX /note= "Specifically referred to in Claim 2"
XX
XX FT 124..129
XX /label= CDR3
XX /note= "Specifically referred to in Claim 2"
XX
XX WO2004003166-A2.
XX
XX 08-JAN-2004.
XX
XX 30-JUN-2003; 2003WO-US020602.
XX
XX 01-JUL-2002; 2002US-00189032.
XX
XX (SAVI-) SAVIENT PHARM INC.
XX
XX Levanon A, Ben-Levy R, Plaksin D, Szanton E, Hagai Y;
XX Hoch Mar- Chaim H;
XX WPI; 2004-203378/19.
XX
XX Novel antibody or its fragment that binds to an epitope of P-Selectin-
XX Glycoprotein Ligand-1, useful for diagnosing/prognosing inflammation,
XX infection, auto-immune disease, metastasis, tumor/leukemia cell in
XX patient.
XX
XX Claim 1; SEQ ID NO 1; 106pp; English.
XX
XX The present sequence is that of an scFv antibody fragment, designated
XX L32, that binds P-selectin glycoprotein ligand-1 (PSGL-1). The antibody
XX was identified by screening a phage library, which had diversity only in
XX the heavy chain CDR3 regions, against a leukaemia cell to select specific
XX antibodies that recognised leukaemia cell surface determinants, wherein
XX the specific receptor was not previously known or characterised. The
XX invention relates to an antibody or its fragment having the binding
XX capabilities of L32. Such antibodies can be used in therapeutic,
XX diagnostic, prognostic and staging methods. Pharmaceutical compositions
XX comprising such antibodies are used to treat conditions related to:
XX inhibiting or treating cell rolling, inflammation, autoimmune disease,
XX infection (e.g. HIV infection), metastasis, and growth and/or replication
XX of tumour cells; increasing the mortality of tumour cells; inhibiting
XX growth and/or replication of tumour cells; inhibiting growth and/or
XX replication of leukaemia cells; increasing the mortality rate of
XX leukaemia cells; altering the susceptibility of diseased cells to damage
XX by anti-disease agents; increasing the susceptibility of tumour cells to
XX damage by anti-cancer agents; increasing the susceptibility of leukaemia
XX cells to damage by anti-leukaemia agents; inhibiting increase in number
XX of tumour cells in a patient; decreasing the number of tumour cells in a
XX patient; inhibiting increase in number of leukaemia cells in a patient;
XX and decreasing the number of leukaemia cells in a patient. Other methods
XX are provided to induce antibody-dependent cell-mediated cytotoxicity or
XX stimulate natural killer or T cells using the antibodies. A method of
XX purging tumour cells from a patient involves incubating the cells with
XX the antibody.
XX
XX Sequence 280 AA;
XX
XX Query Match 96.8%; Score 1393.5; DB 8; Length 280;
XX Best Local Similarity 97.1%; Pred. No. 7e-86;
XX Matches 272; Conservative 0; Mismatches 5; Indels 3; Gaps 1;
QY 1 MKYLLPTAAAGLLLLAAQPAEAQVQLVSGGQVVRPGGSLRLSCAASGFTFD-DYGM5 57
Db 1 MKYLLPTAAAGLLLLAAQPAEAQVQLVSGGQVVRPGGSLRLSCAASGFTFDLNPVKHM 60
```

Qy 58 WVRQAPKGLWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQWNSLRADTAVYY 117
 Db 61 WVRQAPKGLWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQWNSLRADTAVYY 120
 Qy 118 CARMRAPVINGQGLVTVSRGGSGGGGGSGGSELTDPAVSVVALGQTVRITCQGDS 177
 Db 121 CARMRAPVINGQGLVTVSRGGSGGGGGSGGSELTDPAVSVVALGQTVRITCQGDS 180
 Qy 178 LRSYASWYQKPGQAPVLVIYGNKNNPSGTPDRFSGSSGNTASLTITGAQAEDEADYY 237
 Db 181 LRSYASWYQKPGQAPVLVIYGNKNNPSGTPDRFSGSSGNTASLTITGAQAEDEADYY 240
 Qy 238 CNSRDSGNHVVFGGKTLTVLGAARQKLISEEDLNGAA 277
 Db 241 CNSRDSGNHVVFGGKTLTVLGAARQKLISEEDLNGAA 280

RESULT 10
 ADT63078
 ID ADT63078 standard; protein; 280 AA.
 AC ADT63078;
 XX
 DT 13-JAN-2005 (first entry)
 XX
 DE Human scFv antibody fragment binding PSGL-1.
 XX
 KW P-selectin Glycoprotein Ligand-1; PSGL-1; heavy chain;
 KW complementarity determining region; CDR;
 KW T cell-acute lymphoblastic leukaemia cell;
 KW acute myelogenous leukaemia cell; B-leukaemia cell;
 KW B cell-chronic lymphocytic leukaemia; multiple myeloma cell;
 KW tumour cell; HIV infection; auto-immune disease; metastasis;
 KW tumour cell; anti-cancer; cytostatic; antimicrobial; antiinflammatory;
 KW immunosuppressive; anti-HIV; human; scFv antibody fragment.
 XX
 OS Homo sapiens.
 XX
 XX US2004208877-A1.
 XX
 XX 21-OCT-2004.
 XX
 XX 30-JUN-2003; 2003US-00611588.
 XX
 XX 01-JUL-2002; 2002US-0393491P.
 XX
 XX (LEVA/) LEVANON A.
 XX (BENL/) BEN-LEVY R.
 XX (PLAK/) PLAKSIN D.
 XX (SZAN/) SZANTON E.
 XX (HAGA/) HAGAI Y.
 XX (MARC/) MAR-CHAIM H H.
 XX
 XX Levanon A, Ben-Levy R, Plaksin D, Szanton E, Hagai Y;
 XX Mar-Chaim HH;
 XX
 XX WPI; 2004-765453/75.
 XX
 XX New antibody or its fragment that binds to an epitope of P-selectin
 XX Glycoprotein Ligand-1 (PSGL-1), useful for manufacturing a medicament for
 XX treating e.g., inflammation, HIV infection, auto-immune disease, and
 XX metastasis.
 XX
 XX Claim 1; SEQ ID NO 1; 49pp; English.
 XX
 XX The present invention relates to an antibody or its fragment that binds
 XX to an epitope of P-selectin Glycoprotein Ligand-1 (PSGL-1) comprising a
 XX sequence comprising 280 amino acids (SEQ ID NO: 1) fully defined in the
 XX specification, that has the binding capabilities of an scFv of SEQ ID NO:
 XX 1, or comprising one heavy chain complementarity determining region
 XX (CDR). The heavy chain CDR comprises the sequences given in the
 XX specification as SEQ ID NO: 2, 3, or 4. Two or three heavy chain CDRs are
 XX selected from SEQ ID NO: 2, 3, and 4. The antibody or its fragment

CC comprises at least one framework variable region from germline DP32. It
 CC may be a substantially circular or looped peptide or polypeptide. The
 CC epitope comprises at least one sulphated moiety. The antibody or its
 CC fragment may bind or cross-react with two or more epitopes, each epitope
 CC comprising one or more sulphated tyrosine residues, preferably comprising
 CC at least one cluster of two or more acidic amino acids. It may bind to an
 CC epitope on at least one cell selected from T cell-acute lymphoblastic
 CC leukaemia cells, acute myelogenous leukaemia cells, B-leukaemia cells, B
 CC cell-chronic lymphocytic leukaemia, and multiple myeloma cells. It may
 CC bind to an epitope on a lipid, carbohydrate, peptide glycolipid,
 CC glycoprotein, lipoprotein, and/or lipopolysaccharide molecule. It may be
 CC coupled to or complexed with an agent selected from anti-cancer, anti-
 CC leukemic, anti-metastasis, anti-neoplastic, anti-disease, anti-adhesion,
 CC anti-thrombosis, anti-restenosis, anti-autoimmune, anti-aggregation, anti-
 CC bacterial, anti-viral, and anti-inflammatory agents, preferably anti-
 CC viral agent selected from acyclovir, ganciclovir and zidovudine. The
 CC agent may be selected from toxins, radioisotopes, imaging agents, and
 CC pharmaceutical agents. The antibody or its fragment may be coupled to or
 CC complexed with a vehicle or carrier that can be coupled or complexed to
 CC more than one agent. The vehicle or carrier is selected from dextran,
 CC lipophilic polymers, HPMA, and liposomes, and their derivatives and
 CC modifications. A pharmaceutical composition comprising the antibody or
 CC its fragments is useful in a method for treating a disease or cell
 CC rolling in a patient, for ameliorating the effects of inflammation,
 CC preventing inflammation, treating inflammation, or inhibiting the
 CC progress of inflammation, for treating an infection, i.e. caused by HIV,
 CC where the administration prevents cell entry of HIV, for treating an auto-
 CC immune disease, for treating metastasis, or for treating growth and/or
 CC replication of tumour or leukaemia cells. The pharmaceutical composition
 CC is also useful for manufacturing a medicament for treating the diseases.
 CC The pharmaceutical composition is useful for increasing the mortality
 CC rate of tumour or leukaemia cells, altering the susceptibility of
 CC diseased, tumour or leukaemia cells to damage by anti-disease agents or
 CC anti-cancer agents, inhibiting increase in number or decreasing number of
 CC tumour or leukaemia cells in a patient having a tumour or leukaemia,
 CC eliciting antibody dependent cell-mediated cytotoxicity or stimulating a
 CC natural killer cell or a T cell, diagnosing, prognosing or staging a
 CC metastasis, tumour cell, or leukaemia in a patient, or for purging tumour
 CC cells from a patient. The present sequence represents a human scFv
 CC antibody fragment that binds to an epitope of PSGL-1.
 XX
 XX Sequence 280 AA;

Query Match 96.8%; Score 1393.5; DB 8; Length 280;
 Best Local Similarity 97.1%; Pred. No. 7e-86;
 Matches 272; Conservative 0; Mismatches 5; Indels 3; Gaps 1;
 Qy 1 MKYLLPTAAAGLLLLAAQPAEAQVQLVESGQGVVRRPGSLRLSCAASGFTFD---DYGMS 57
 Db 1 MKYLLPTAAAGLLLLAAQPAEAQVQLVESGQGVVRRPGSLRLSCAASGFTFDLNPVKHM 60
 Qy 58 WVRQAPKGLWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQWNSLRADTAVYY 117
 Db 61 WVRQAPKGLWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQWNSLRADTAVYY 120
 Qy 118 CARMRAPVINGQGLVTVSRGGSGGGSGGSELTDPAVSVVALGQTVRITCQGDS 177
 Db 121 CARMRAPVINGQGLVTVSRGGSGGGSGGSELTDPAVSVVALGQTVRITCQGDS 180
 Qy 178 LRSYASWYQKPGQAPVLVIYGNKNNPSGTPDRFSGSSGNTASLTITGAQAEDEADYY 237
 Db 181 LRSYASWYQKPGQAPVLVIYGNKNNPSGTPDRFSGSSGNTASLTITGAQAEDEADYY 240
 Qy 238 CNSRDSGNHVVFGGKTLTVLGAARQKLISEEDLNGAA 277
 Db 241 CNSRDSGNHVVFGGKTLTVLGAARQKLISEEDLNGAA 280

RESULT 11
 ADX01131
 ID ADX01131 standard; protein; 280 AA.
 XX
 XX ADX01131;
 AC

XX 21-APR-2005 (first entry)
 XX Amino acid sequence for scFv antibody, SEQ ID NO:6.
 XX
 XX antibody; cancer; diagnosis; tumor; HIV infection; autoimmune disease;
 XX metastasis; leukemia; platelet; antiaggregant; restenosis;
 XX antibody dependent cell-mediated cytotoxicity; apoptosis;
 XX natural killer cell; T-lymphocyte; inflammation; cardiovascular disease;
 XX retinopathy; anti-HIV; cytostatic; immunosuppressive; antiinflammatory;
 XX cardiovascular-gen.; ophthalmological; scFv.
 XX Unidentified.
 XX W02005010153-A2.
 XX
 XX 03-FEB-2005.
 XX
 XX 30-JUN-2004; 2004WO-US021002.
 XX
 XX 30-JUN-2003; 2003US-00611238.
 XX
 XX (SAVI-) SAVIENT PHARM INC.
 XX
 XX Plaksin D, Levanon A, Szanton E, Hagay Y, Ben-Levy R, Nisgav Y;
 XX Szrajber T, Kanfi Y;
 XX WPI; 2005-132536/14.
 XX
 XX Novel antibody e.g., S15 antibody or their fragments useful for purging
 XX tumor cells from patient or for treating autoimmune disease,
 XX inflammatory diseases, cardiovascular diseases or retinopathic diseases.
 XX
 XX Claim 14; SEQ ID NO 6; 134pp; English.
 XX
 XX The invention relates to antibodies e.g. S15 antibody, or their fragments
 XX that bind to cancer cells. The antibodies or their fragments comprise a
 XX consensus sequence (given as SEQ ID NO:3 in the specification) of X1-X2-
 XX X3-Pro-X5-X6, where X1 and X6 are hydrophobic amino acids and X2, X3 and
 XX X5 are any amino acid. Also described are (i) a composition comprising
 XX the antibody and a carrier, (ii) a diagnostic, prognostic or staging kit
 XX comprising the antibody and an imaging agent, (iii) an isolated or
 XX purified DNA sequence encoding the antibody, (iv) an expression vector
 XX comprising the DNA sequence, (v) a recombinant host cell comprising the
 XX expression vector, (vi) a method of producing the antibody, (vii) a
 XX polypeptide comprising the consensus sequence, (viii) a method of
 XX selecting an antibody or their fragments or a polypeptide, (ix) an
 XX antibody or their fragment produced by the method, (x) a library of
 XX immunoglobulin binding domains, (xi) a small inorganic molecule that
 XX binds to a sulfated epitope of pSGL-1, GP1b and/or CCR5, and (xii) a
 XX composition comprising a small inorganic molecule. The antibody of the
 XX invention is useful for diagnosing, prognosing, or staging a disease in a
 XX patient which involves providing a sample containing a cell from the
 XX patient and determining whether the antibody binds to the cell of the
 XX patient, thus indicating that the patient is at risk or has the disease.
 XX The antibody is useful for purging tumor cells from a patient which
 XX involves providing a sample containing cells from the patient, and
 XX incubating the cells from the patient with the antibody, where purging
 XX occurs under ex vivo conditions. A composition comprising the antibody is
 XX useful for treating a disease (e.g. infection caused by HIV) or cell
 XX killing, inhibiting autoimmune disease, metastasis or growth and/or
 XX replication of tumor or leukemic cells e.g. B-CLL cells, increasing the
 XX mortality rate of tumor or leukemic cells, altering the susceptibility of
 XX disease cells to damage by anti-disease agents, increasing the
 XX susceptibility of tumor or leukemic cells to damage by anticancer or
 XX antileukemic agents, inhibiting platelet aggregation or restenosis,
 XX eliciting antibody dependent cell-mediated cytotoxicity (ADCC), eliciting
 XX apoptosis in leukemic cells, or stimulating a natural killer (NK) cell or
 XX a T cell. ADCC is mediated by effector cells e.g. natural killer or
 XX monocytic cells. The composition is also useful for producing medicament
 XX for treating a disease. The library of immunoglobulin binding domains is
 XX useful for selecting a sulfated epitope that binds to the antigen-binding
 XX domain. The antibody is useful for treating cancer, leukemia, autoimmune

CC diseases, inflammatory diseases, HIV infection, cardiovascular diseases,
 CC and retinopathic diseases. This sequence represents a scFv antibody.
 XX
 XX SQ Sequence 280 AA;
 XX
 XX Query Match 96.4%; Score 1388.5; DB 9; Length 280;
 XX Best Local Similarity 96.8%; Pred. No. 1.5e-85;
 XX Matches 271; Conservative 0; Mismatches 6; Indels 3; Gaps 1;
 QY 1 MKYLLPTAAGLGLLLAAQPAEAQVQLVESGGGVVRRPGSLRLSCAASGFTD---DYGMS 57
 DB 1 MKYLLPTAAGLGLLLAAQPAEAQVQLVESGGGVVRRPGSLRLSCAASGFTDLDLPKVKGM 60
 QY 58 WVRQAPGKGLWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYY 117
 DB 61 WVRQAPGKGLWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYY 120
 QY 118 CARMRAPVTWGQGLTVTSRGG 177
 DB 121 CARMRAPVTWGQGLTVTSRGG 180
 QY 178 LRSYASWYQKPGQAPVLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEADYY 237
 DB 181 LRSYASWYQKPGQAPVLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEADYY 240
 QY 238 CNSRDSGNNHVPFGGQTKLTVLGAAGAEQKLISEEDLNGAA 277
 DB 241 CNSRDSGNNHVPFGGQTKLTVLGAAGAEQKLISEEDLNGAA 280

RESULT 12
 ADY78325
 ID ADY78325 standard; protein; 280 AA.
 XX
 XX AC ADY78325;
 XX
 XX DT 16-JUN-2005 (first entry)
 XX
 XX DE Single chain Fv antibody SEQ ID NO:6.
 XX
 XX KW antibody; metastasis; cancer; autoimmune disease; cytostatic; anti-HIV;
 XX antiinflammatory; immunosuppressive; vasotropic; cardiovascular-gen.;
 XX cardiant; infection; inflammation; leukemia; Fv.
 XX
 XX OS Synthetic.
 XX
 XX PN US2005069955-A1.
 XX
 XX PD 31-MAR-2005.
 XX
 XX PF 30-JUN-2004; 2004US-00880922.
 XX
 XX PR 30-JUN-2003; 2003US-0484061P.
 XX
 XX PA (BLAK/) PLAKSIN D.
 XX PA (LEVA/) LEVANON A.
 XX PA (SZAN/) SZANTON E.
 XX PA (HAGA/) HAGAY Y.
 XX PA (BENL/) BEN-LEVY R.
 XX PA (NISG/) NISGAV Y.
 XX PA (KANF/) KANFI Y.
 XX
 XX PI Plaksin D, Levanon A, Szanton E, Hagay Y, Ben-Levy R, Nisgav Y;
 XX Kanfi Y;
 XX
 XX DR WPI; 2005-261644/27.
 XX
 XX PT Novel antibody or its fragment comprising consensus sequence that binds
 XX to cancer cell, useful for diagnosing or treating diseases such as
 XX cancer, autoimmune diseases and inflammatory diseases.
 XX
 XX PS Claim 14; SEQ ID NO 6; 74pp; English.
 XX

CC The invention relates to an antibody or its fragment (I) comprising the
 CC consensus sequence X1-X2-X3-Pro-X5-X6, where X1 and X6 are hydrophobic
 CC amino acids and X2, X3 and X5 are any amino acid. Also described: (1) a
 CC pharmaceutical composition (II), comprising (I) and a carrier; (2) a
 CC diagnostic, prognostic, or staging kit (K1), comprising (I) and an
 CC imaging agent; (3) an isolated or purified DNA sequence (III) encoding
 CC host cell (V) comprising (IV) comprising (III); (5) a recombinant
 CC immunoglobulin binding domain, comprising (I); (7) a library (VII) of
 CC domain for complementary binding, where (VII) has diversity only in heavy
 CC chain CDR3; (8) a small inorganic molecule (VIII) capable of binding to a
 CC sulfated epitope of PSG1-1, GF1b, and/or CCR5; and (9) a pharmaceutical
 CC composition (IX), comprising (VIII). (II) is useful for treating a
 CC disease, cell rolling, an infection (where the infection is caused by HIV
 CC and the administration of (II) prevents entry of HIV), and inflammation.
 CC (II) can also be used for inhibiting autoimmune disease, inhibiting
 CC metastasis, inhibiting growth and/or replication of tumor cells, and/or
 CC increasing the mortality rate of tumor cells, inhibiting growth and/or
 CC replication of leukemia cells, increasing the mortality rate of leukemia
 CC cells, inhibiting growth and/or replication of B-CLL cells, altering the
 CC susceptibility of diseased cells to damage by anti-cancer agents,
 CC increasing the susceptibility of leukemia cells to damage by anti-
 CC leukemia agents, increasing the susceptibility of B-CLL cells to damage
 CC by anti-leukemia agents, inhibiting platelet aggregation, inhibiting
 CC restenosis, eliciting antibody dependent cell-mediated cytotoxicity
 CC (ADCC) mediated by effector cells comprising of natural killer (NK) or
 CC monocytic cells), eliciting apoptosis in leukemia cells, stimulating a NK
 CC cell or a T cell, and manufacturing medicament for treating a disease.
 CC (I) is useful for diagnosing, prognosing or staging a disease in a
 CC patient, which involves providing a sample containing a cell from the
 CC patient and determining whether (I) binds to the cell of the patient, and
 CC so indicates that the patient is at risk for or has the disease. (I) is
 CC useful for purging tumor cells from a patient, which involves providing a
 CC sample containing cells from the patient and incubating the cells from
 CC the patient with (I), where the purging occurs ex vivo. (VII) is useful
 CC for selecting a sulfated epitope, which involves providing (VII), panning
 CC (VII) for a sulfated epitope that binds to the antigen binding domain,
 CC and isolating the sulfated epitope. (V) is useful for producing (I). (II)
 CC is useful for treating cardiovascular diseases such as myocardial
 CC infarction and inflammatory diseases. The present sequence represents a
 CC scFv antibody from the present invention.

XX Sequence 280 AA;

Query Match 96.4%; Score 1388.5; DB 9; Length 280;
 Best Local Similarity 96.8%; Pred. No. 1.5e-85;
 Matches 271; Conservative 0; Mismatches 6; Indels 3; Gaps 1;
 Qy 1 MKYLLPTAAAGLLLLAQAQPAEAQVQLVSGGVRPGGSLRLSCAASGFTFD---DYGMS 57
 Db 1 MKYLLPTAAAGLLLLAQAQPAEAQVQLVSGGVRPGGSLRLSCAASGFTFDLNPVKVHM 60
 Qy 58 WYQAPGKLEWVSGINWNGSGTGYADSVKGRFTISRDNAKNSLYLQNSLRADTVAYY 117
 Db 61 WYQAPGKLEWVSGINWNGSGTGYADSVKGRFTISRDNAKNSLYLQNSLRADTVAYY 120
 Qy 118 CARMRAPVWGQGTFLVTVSRGGSGGGGGSSSELTQDPVAVSVALGQTVRITTCGDS 177
 Db 121 CARMRAPVWGQGTFLVTVSRGGSGGGGGSSSELTQDPVAVSVALGQTVRITTCGDS 180
 Qy 178 LRSYASWYQKPGQAPVLYVIGNKRRPSGIPDRFGSSSGNTASLTITGAQAEADYY 237
 Db 181 LRSYASWYQKPGQAPVLYVIGNKRRPSGIPDRFGSSSGNTASLTITGAQAEADYY 240
 Qy 238 CNSRDSGNHVVFGGKTLVLGAAAEQKLISEEDINGAA 277
 Db 241 CNSRDSGNHVVFGGKTLVLGAAAEQKLISEEDINGAA 280

RESULT 13

ID ADI28368

AD I28368 standard; protein; 280 AA.

XX

AC ADI28368;

XX 06-MAY-2004 (first entry)

XX Human scFv fragment L32, binds to leukaemia cells.

XX Human; antibody; scFv; leukaemia; drug delivery; cancer; therapy.

XX Homo sapiens.

XX WO2004002528-A1.

XX 08-JAN-2004.

XX 30-JUN-2003; 2003WO-US020604.

XX 01-JUL-2002; 2002US-00189025.

XX (SAVI-) SAVIENT PHARM INC.

XX Lazarovits J, Nimrod A, Hoch-Mar-Chaim H, Levanon A;

XX WPI; 2004-099189/10.

XX Composition comprising an agent and/or antibody or its fragment, useful
 XX for treating auto-immune disease, thrombosis, restenosis, metastasis, or
 XX for inhibiting growth and/or replication of tumor cells or leukemia
 XX cells.

XX Claim 13; SEQ ID NO 3; 58pp; English.

XX The present sequence is the protein sequence of human scFv fragment L32.
 XX This antibody was identified by screening a human antibody phage library
 XX that has diversity only in the heavy chain CDR3 regions. Leukemia cells
 XX were screened to select specific antibodies that recognise leukemia cells
 XX surface determinants. The invention relates to compositions utilising an
 XX agent and an antibody or its fragment. The agent is a toxin, radioisotope
 XX or pharmaceutical agent such as doxorubicin. It is complexed or combined
 XX with or conjugated to the antibody or its fragment. The agent and/or
 XX antibody can be present in the composition is a sub-clinical amount, i.e.
 XX less than the amount generally found to be clinically effective when the
 XX agent is administered alone. The composition is used in claimed methods
 XX of: inhibiting cell rolling, inflammation, thrombosis, restenosis,
 XX metastasis, the growth and/or replication of tumour cells or leukaemia
 XX cells, an increase in number of tumour or leukaemia cells, cell-cell,
 XX cell-matrix, platelet-matrix, platelet-platelet and/or cell-platelet
 XX complex formation, aggregation or adhesion; increasing the mortality rate
 XX of tumour or leukaemia cells, the susceptibility of disease cells to
 XX damage by anti-disease agents, and the susceptibility of tumour or
 XX leukaemia cells to damage by anti-cancer agents; and ameliorating the
 XX effects of a disease, preventing a disease, treating a disease or
 XX inhibiting the progress of a disease.

XX Sequence 280 AA;

Query Match 96.3%; Score 1386.5; DB 8; Length 280;
 Best Local Similarity 96.8%; Pred. No. 2.1e-85;
 Matches 271; Conservative 0; Mismatches 6; Indels 3; Gaps 1;
 Qy 1 MKYLLPTAAAGLLLLAQAQPAEAQVQLVSGGVRPGGSLRLSCAASGFTFD---DYGMS 57
 Db 1 MKYLLPTAAAGLLLLAQAQPAEAQVQLVSGGVRPGGSLRLSCAASGFTFDLNPVKVHM 60
 Qy 58 WYQAPGKLEWVSGINWNGSGTGYADSVKGRFTISRDNAKNSLYLQNSLRADTVAYY 117
 Db 61 WYQAPGKLEWVSGINWNGSGTGYADSVKGRFTISRDNAKNSLYLQNSLRADTVAYY 120
 Qy 118 CARMRAPVWGQGTFLVTVSRGGSGGGGGSSSELTQDPVAVSVALGQTVRITTCGDS 177
 Db 121 CARMRAPVWGQGTFLVTVSRGGSGGGGGSSSELTQDPVAVSVALGQTVRITTCGDS 180
 Qy 178 LRSYASWYQKPGQAPVLYVIGNKRRPSGIPDRFGSSSGNTASLTITGAQAEADYY 237
 Db 178 LRSYASWYQKPGQAPVLYVIGNKRRPSGIPDRFGSSSGNTASLTITGAQAEADYY 237

Db 181 LRSYASWYQKPGQAPVLVIYGNKRNPSGIPDRFSGSSSGNTASLTITGAQAEDEADYY 240

QY 238 CNSRDSGNHVVFGGKTLTVLGAAAEQKLISEEDLNGAA 277
 |||||
 Db 241 CNSRDSGNHVVFGGKTLTVLGAAAEQKLISEEDLNGAA 280
 |||||

RESULT 14
 ADS82028
 ID ADS82028 standard; protein; 280 AA.

XX AC ADS82028;
 XX DT 30-DEC-2004 (first entry)
 XX Human leukaemia cell binding scFv antibody fragment L32.

XX cell rolling; inflammation; autoimmune disease; thrombosis; restenosis;
 KW metastasis; tumour; leukaemia; cardiovascular disease; retinopathy;
 KW human; scFv; antibody; cytostatic; antiinflammatory; thrombolytic;
 KW vasotropic; immunosuppressive; cardiovascular-Gen; ophthalmological.

XX Homo sapiens.

XX US2004202665-A1.
 XX 14-OCT-2004.

XX 30-JUN-2003; 2003US-00610843.
 XX 01-JUL-2002; 2002US-0393453P.

XX (LAZA/) LAZAROVITS J.
 PA (NIME/) NIMROD A.
 PA (HOCH/) HOCH M H.
 PA (LEVA/) LEVANON A.

XX Lazarovits J, Nimrod A, Hoch MH, Levanon A;
 WPI; 2004-746943/73.

XX Composition useful for treating diseases e.g., inflammatory diseases,
 PT thrombosis, restenosis, autoimmune diseases, cardiovascular diseases or
 PT retinopathic diseases, comprises agent and antibody or its fragment.

XX Claim 13; SEQ ID NO 3; 22pp; English.

XX The invention relates to a composition which comprises an agent and an
 CC antibody or its fragment. The composition is useful for inhibiting cell
 CC rolling, inflammation, autoimmune disease, thrombosis, restenosis,
 CC metastasis, cell-cell, cell-matrix, platelet-matrix, platelet-platelet
 CC and/or cell-platelet complex formation, aggregation or adhesion, increase
 CC in number of tumour cells or growth and/or replication of tumour or
 CC leukaemia cells, for increasing the mortality rate of tumour or leukaemia
 CC cells, the susceptibility of tumour or leukaemia cells to damage by anti-
 CC cancer agents, for decreasing number of tumour or leukaemia cells, or for
 CC ameliorating the effect of a disease, preventing a disease, treating a
 CC disease, or inhibiting the progress of a disease. The composition is
 CC useful for therapeutic treatment, where antibody or its fragment and the
 CC agent are administered separately. The antibody or its fragment is
 CC administered prior to or subsequent to the agent. The composition is
 CC useful for treating diseases such as inflammatory diseases, diseases
 CC involving abnormal or pathogenic adhesion, thrombosis and/or restenosis,
 CC diseases involving abnormal or pathogenic aggregation, autoimmune
 CC diseases, cardiovascular diseases, retinopathic diseases, diseases caused
 CC by sulphated tyrosine-dependent protein-protein interactions or diseased
 CC cells. The present sequence represents the human leukaemia cell binding
 CC scFv antibody fragment L32.

XX Sequence 280 AA;
 SQ

Query Match 96.3%; Score 1386.5; DB 8; Length 280;
 Best Local Similarity 96.8%; Pred. No. 2.1e-85;

Matches 271; Conservative 0; Mismatches 6; Indels 3; Gaps 1;

QY 1 MKYLLPTAAAGLLLLAAQPAEAQVQVVGSGGVVRRPGSLRLSCAASGFTFD--DYGMS 57
 |||||
 Db 1 MKYLLPTAAAGLLLLAAQPAEAQVQVVGSGGVVRRPGSLRLSCAASGFTFDLNPVKHM 60
 |||||

QY 58 WYRQAPKGLIEWVSGINWNGSGTYADSVKGRFTISRDNKNSLYLQMSLRADETAVYY 117
 |||||
 Db 61 WYRQAPKGLIEWVSGINWNGSGTYADSVKGRFTISRDNKNSLYLQMSLRADETAVYY 120
 |||||

QY 118 CARMRAPVIWGQTLTVTSRGGGGGGGGGGSSSELTDQPAVSVALGQTVRITCGDS 177
 |||||
 Db 121 CARMRAPVIWGQTLTVTSRGGGGGGGGGGSSSELTDQPAVSVALGQTVRITCGDS 180
 |||||

QY 178 LRSYASWYQKPGQAPVLVIYGNKRNPSGIPDRFSGSSSGNTASLTITGAQAEDEADYY 237
 |||||
 Db 181 LRSYASWYQKPGQAPVLVIYGNKRNPSGIPDRFSGSSSGNTASLTITGAQAEDEADYY 240
 |||||

QY 238 CNSRDSGNHVVFGGKTLTVLGAAAEQKLISEEDLNGAA 277
 |||||
 Db 241 CNSRDSGNHVVFGGKTLTVLGAAAEQKLISEEDLNGAA 280
 |||||

RESULT 15
 ADX01181
 ID ADX01181 standard; protein; 280 AA.

XX AC ADX01181;
 XX DT 21-APR-2005 (first entry)

XX Amino acid sequence for scFv antibody, SEQ ID No:56.

XX antibody; cancer; diagnosis; tumor; HIV infection; autoimmune disease;
 KW metastasis; leukemia; platelet; antiaggregant; restenosis;
 KW antibody dependent cell-mediated cytotoxicity; apoptosis;
 KW natural killer cell; T-lymphocyte; inflammation; cardiovascular disease;
 KW retinopathy; anti-HIV; cytostatic; immunosuppressive; antiinflammatory;
 KW cardiovascular-gen.; ophthalmological; scFv.

XX Unidentified.

XX WO2005010153-A2.
 XX 03-FEB-2005.

XX 30-JUN-2004; 2004WO-US021002.
 XX 30-JUN-2003; 2003US-00611238.

XX (SAVI-) SAVIENT PHARM INC.

XX Plaksin D, Levanon A, Szanton E, Hagay Y, Ben-Levy R, Nisgav Y;
 PI Srajer T, Kanfi Y;
 XX WPI; 2005-132536/14.

XX Novel antibody e.g., S15 antibody or their fragments useful for purging
 PT tumor cells from patient or for treating autoimmune diseases,
 PT inflammatory diseases, cardiovascular diseases or retinopathic diseases.

XX Claim 14; SEQ ID NO 56; 134pp; English.

XX The invention relates to antibodies e.g. S15 antibody, or their fragments
 CC that bind to cancer cells. The antibodies or their fragments comprise a
 CC consensus sequence (given as SEQ ID No:3 in the specification) of X1-X2-
 CC X3-Pro-X5-X6, where X1 and X6 are hydrophobic amino acids and X2, X3 and
 CC X5 are any amino acid. Also described are (i) a composition comprising
 CC the antibody and a carrier, (ii) a diagnostic, prognostic or staging kit
 CC comprising the antibody and an imaging agent, (iii) an isolated or
 CC purified DNA sequence encoding the antibody, (iv) an expression vector
 CC comprising the DNA sequence, (v) a recombinant host cell comprising the
 CC expression vector, (vi) a method of producing the antibody, (vii) a

polypeptide comprising the consensus sequence, (viii) a method of selecting an antibody or their fragments or a polypeptide, (ix) an antibody or their fragment produced by the method, (x) a library of immunoglobulin binding domains, (xi) a small inorganic molecule that binds to a sulfated epitope of PSGL-1, GPIb and/or CCR5, and (xii) a composition comprising a small inorganic molecule. The antibody of the invention is useful for diagnosing, prognosing, or staging a disease in a patient which involves providing a sample containing a cell from the patient and determining whether the antibody binds to the cell of the patient, thus indicating that the patient is at risk or has the disease. The antibody is useful for purging tumor cells from a patient which involves providing a sample containing cells from the patient, and incubating the cells from the patient with the antibody, where purging occurs under ex vivo conditions. A composition comprising the antibody is useful for treating a disease (e.g. infection caused by HIV) or cell rolling, inhibiting autoimmune disease, metastasis or growth and/or replication of tumor or leukemic cells e.g. B-CLL cells, increasing the mortality rate of tumor or leukemic cells, altering the susceptibility of disease cells to damage by anti-disease agents, increasing the susceptibility of tumor or leukemic cells to damage by anticancer or antileukemic agents, inhibiting platelet aggregation or restenosis, eliciting antibody dependent cell-mediated cytotoxicity (ADCC), eliciting apoptosis in leukemic cells, or stimulating a natural killer (NK) cell or a T cell. ADCC is mediated by effector cells e.g. natural killer or monocytic cells. The composition is also useful for producing medicament for treating a disease. The library of immunoglobulin binding domains is useful for selecting a sulfated epitope that binds to the antigen-binding domain. The antibody is useful for treating cancer, leukemia, autoimmune diseases, inflammatory diseases, HIV infection, cardiovascular diseases, and retinopathic diseases. This sequence represents a scFv antibody.

XX SQ Sequence 280 AA;

Query Match		95.8%;	Score 1379.5;	DB 9;	Length 280;
Best Local Similarity		95.7%;	Pred. No. 6.2e-85;		
Matches 268;		Conservative 2;	Mismatches 7;	Indels 3;	Gaps 1;
Qy	1	MKYLLPTAAAGLLLLAAQPA	MAEVQLVESGGGVVPRPGGSLRLSCAASGFTPD---	DYGMS	57
Db	1	MKYLLPTAAAGLLLLAAQPA	MAEVQLVESGGGVVPRPGGSLRLSCAASGFTFDLNPVKHM	60	
Qy	58	WVROAPGKLEWVSGINWNGSTGYADSVKGRFTISRDN	AKNSLYLQWNSLR	AEDTAVYY	117
Db	61	WVROAPGKLEWVSGINWNGSTGYADSVKGRFTISRDN	AKNSLYLQWNSLR	AEDTAVYY	120
Qy	118	CARMRAPIVTCQGTLTVT	SRGGSGGGSGGSSSELTQDP	PAVSVALGQTVRITCQGS	177
Db	121	CARLVPFLMGQGTLTVT	SRGGSGGGSGGSSSELTQDP	PAVSVALGQTVRITCQGS	180
Qy	178	LSRYASWYQKPGQAPVLIY	GKNNRPSGIPDRFSGSSSGNTASLTITGAQAE	DEADYY	237
Db	181	LSRYASWYQKPGQAPVLIY	GKNNRPSGIPDRFSGSSSGNTASLTITGAQAE	DEADYY	240
Qy	238	CNSRDSSGNHVFGGGTKLTVL	GAAAEQKLI	SEEDLN	277
Db	241	CNSRDSSGNHVFGGGTKLTVL	GAAAEQKLI	SEEDLN	280

Search completed: November 18, 2005, 21:46:17
Job time : 155.792 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 18, 2005, 21:40:23 ; Search time 38.011 Seconds
(without alignments)
602.487 Million cell updates/sec

Title: US-10-029-926D-25

Perfect score: 1440

Sequence: 1 MKYLLPTAAAGLLLLAAQA.....VLGAAAEQKLISEDLNGAA 277

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1278.5	88.8	280	2	US-09-260-527-1
2	1275.5	88.6	309	2	US-09-079-029-9
3	1194	82.9	312	2	US-09-079-029-10
4	1126.5	78.2	278	2	US-09-260-527-3
5	973	67.6	310	2	US-09-079-029-11
6	961.5	66.8	288	2	US-09-818-247-22
7	836.5	58.1	284	2	US-08-564-164A-2
8	829	57.6	282	1	US-08-860-174A-10
9	822	57.1	268	2	US-09-976-118-1
10	803	55.8	240	2	US-09-132-854-2
11	800	55.8	240	2	US-09-511-939-2
12	800	55.6	289	2	US-09-184-658-63
13	800	55.6	289	2	US-09-504-262D-63
14	797.5	55.4	334	2	US-09-646-028-53
15	797.5	55.4	339	2	US-09-646-028-55
16	791.5	55.0	348	2	US-09-646-028-51
17	787.5	54.7	245	2	US-08-918-148-75
18	787.5	54.7	245	2	US-09-138-091A-73
19	786.5	54.6	245	2	US-08-918-148-76
20	786.5	54.6	245	2	US-09-138-091A-74
21	786	54.6	255	2	US-09-553-498-8
22	786	54.6	255	2	US-09-618-869-8
23	781.5	54.3	245	2	US-08-918-148-78
24	781.5	54.3	245	2	US-09-138-091A-76
25	775	53.8	272	2	US-09-726-219A-183
26	775	53.8	272	2	US-09-196-522-183
27	772.5	53.6	301	1	US-08-661-052-14

Sequence 14, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 178, App
Sequence 178, App
Sequence 178, App
Sequence 38, Appl
Sequence 77, Appl
Sequence 75, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 9, Appl
Sequence 44, Appl
Sequence 7, Appl
Sequence 5, Appl
Sequence 78, Appl
Sequence 3, Appl

28 772.5 53.6 301 2 US-09-188-082-14
29 772.5 53.6 301 2 US-09-364-088-14
30 772.5 53.6 301 2 US-09-102-716-14
31 761 52.8 281 2 US-09-025-769B-178
32 761 52.8 281 2 US-09-490-070A-178
33 761 52.8 281 2 US-09-490-153-178
34 761 52.8 281 2 US-09-490-324-178
35 758 52.6 288 2 US-09-423-439-38
36 757 52.6 244 2 US-08-918-148-77
37 757 52.6 244 2 US-09-138-091A-75
38 745.5 51.8 267 2 US-09-485-737B-2
39 745.5 51.8 267 2 US-10-071-485-2
40 744.5 51.7 402 1 US-08-491-988-9
41 742.5 51.6 281 2 US-09-423-439-44
42 739.5 51.4 415 1 US-08-491-988-7
43 739.5 51.4 435 1 US-08-491-988-5
44 737.5 51.2 289 1 US-08-428-257A-72
45 737.5 51.2 269 1 US-08-491-988-3

ALIGNMENTS

RESULT 1

US-09-260-527-1

; Sequence 1, Application US/09260527A

; Patent No. 6228599

; GENERAL INFORMATION:

; APPLICANT: Knox, J.P.

; APPLICANT: Mikkelsen, J.D.

; APPLICANT: Willats, W. G.

; TITLE OF INVENTION: ANTIBODY

; FILE REFERENCE: DY0U19.001AUS

; CURRENT APPLICATION NUMBER: US/09/260,527A

; CURRENT FILING DATE: 1999-02-26

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 280

; TYPE: PRT

; ORGANISM: UNKNOWN

; FEATURE:

; OTHER INFORMATION: Anti-homogalacturonan specific antibodies from a

; OTHER INFORMATION: phage display library known as the Synthetic scFv

; OTHER INFORMATION: Library (#1) from the Centre for Protein

; OTHER INFORMATION: Engineering, MRC Centre, Cambridge, UK.

US-09-260-527-1

Query Match 88.8%; Score 1278.5; DB 2; Length 280;

Best Local Similarity 90.0%; Pred. No. 5.7e-96;

Matches 252; Conservative 10; Mismatches 15; Indels 3; Gaps 2;

Qy 1 MKYLLPTAAAGLLLLAAQAQMAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDYGMWVR 60

Db 1 MKYLLPTAAAGLLLLAAQAQMAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDYGMWVR 60

Qy 61 QAPKGLEWVSGI--NWNGSGTCYADSVKGRFTISRDNAKNSLYLQWNSLRADETAVYVC 118

Db 61 QAPKGLEWVSGI--NWNGSGTCYADSVKGRFTISRDNAKNSLYLQWNSLRADETAVYVC 120

Qy 119 AR-MRAPVINGQGTLTVTVSRRGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGG 177

Db 119 AR-MRAPVINGQGTLTVTVSRRGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGG 180

Qy 178 LRSYASWYQKQGPAPVLVIYKNNRPSGIPDRFGSSSGNTASLTITGAQAEADYY 237

Db 181 LRSYASWYQKQGPAPVLVIYKNNRPSGIPDRFGSSSGNTASLTITGAQAEADYY 240

Qy 238 CNSRDSGNHVFVGGGTKLTVLGAAAEQKLISEDLNGAA 277

Db 241 CNSRDSGNHVFVGGGTKLTVLGAAAEQKLISEDLNGAA 280

RESULT 2

US-09-079-029-9
; Sequence 9, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marchang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-079-029-9

Query Match 88.6%; Score 1275.5; DB 2; Length 309;
Best Local Similarity 89.9%; Pred. No. 1.1e-95;
Matches 249; Conservative 5; Mismatches 8; Indels 15; Gaps 2;

Qy 16 AAQPMALVQLVSGGGVVRPGGSLRLSCAASGFTPDYGMVSRQAPGKLEWVSGINW 75
Db 33 AAQPMALVQLVSGGGVVRPGGSLRLSCAASGFTPDYGMVSRQAPGKLEWVSGINW 92

Qy 76 NGSTGYADSVKGRFTISRDNKNSLYLQNSLRAEDTAVYICARMAP-----VIWQQ 129
Db 93 NGSTGYADSVKGRFTISRDNKNSLYLQNSLRAEDTAVYICAKILGAGRWYFDLWGK 152

Qy 130 GTLVVSRGGGGGGGGGGSSSELTPDPAVSVALGQTVRITCGDLSLSYASWYQOK 189
Db 153 GTTVVSRGGGGGGGGGGSSSELTPDPAVSVALGQTVRITCGDLSLSYASWYQOK 212

Qy 190 PQQAPVLVIYGNKRPFGIPDRFGSSSGNTASLTITGAQAEADYICNSRDSGNHVV 249
Db 213 PQQAPVLVIYGNKRPFGIPDRFGSSSGNTASLTITGAQAEADYICNSRDSGNHVV 272

Qy 250 FGGTGTTLVGLA-----AAEQKLISEEDLNGAA 277
Db 273 FGGTGTTLVGLAHHHHAABQKLISEEDLNGAA 309

RESULT 3

US-09-079-029-10
; Sequence 10, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Chuntharapai, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marchang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-079-029-10

Query Match 82.9%; Score 1194; DB 2; Length 312;
Best Local Similarity 85.0%; Pred. No. 4.6e-89;
Matches 238; Conservative 5; Mismatches 19; Indels 18; Gaps 2;

Qy 16 AAQPMALVQLVSGGGVVRPGGSLRLSCAASGFTPDYGMVSRQAPGKLEWVSGINW 75
Db 33 AAQPMALVQLVSGGGVVRPGGSLRLSCAASGFTPDYGMVSRQAPGKLEWVSGINW 92

Qy 76 NGSTGYADSVKGRFTISRDNKNSLYLQNSLRAEDTAVYICARMAPY-----I 126
Db 93 DSGEYTVDSVKGRTISRDNKNSLYLQNSLRAEDTAVYICARDLLKYGSSSGWFDP 152

Qy 127 WGGTTLVTVSRGGGGGGGGSSSELTPDPAVSVALGQTVRITCGDLSLSYASWY 186
Db 153 WGGTTLVTVSRGGGGGGGGSSSELTPDPAVSVALGQTVRITCGDLSLSYASWY 212

Qy 187 QQKPGQAPVLVIYGNKRPFGIPDRFGSSSGNTASLTITGAQAEADYICNSRDSGN 246
Db 213 QQKPGQAPVLVIYGNKRPFGIPDRFGSSSGNTASLTITGAQAEADYICNSRDSGN 272

Qy 247 HVVPGGGTTLVGLA-----AAEQKLISEEDLNGAA 277
Db 273 HVVPGGGTTLVGLAHHHHAABQKLISEEDLNGAA 312

RESULT 4

US-09-260-527-3
; Sequence 3, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
; APPLICANT: Knox, J.P.
; APPLICANT: Mikkelsen, J.D.
; APPLICANT: Willats, W.G.
; TITLE OF INVENTION: ANTIBODY
; FILE REFERENCE: DYOUI9.001AUS
; CURRENT APPLICATION NUMBER: US/09/260,527A
; CURRENT FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 3
LENGTH: 278
TYPE: PRT
ORGANISM: UNKNOWN
FEATURE:
OTHER INFORMATION: Anti-homogalacturonan specific antibodies selected
OTHER INFORMATION: from a naive phage display library known as the
OTHER INFORMATION: Synthetic scFv Library (#1) from the Centre for
OTHER INFORMATION: Protein Engineering, MRC Centre, Cambridge, UK
US-029-260-527-3

Query Match 78.2%; Score 1126.5; DB 2; Length 278;
Best Local Similarity 80.3%; Pred. NO. 1.2e-83;
Matches 224; Conservative 17; Mismatches 35; Indels 3; Gaps 3;

QY 1 MKYLLPTAAAGLLLLAAQAPMAAEVOLVESGGVVRPGSLRLSCAASGFTDDYGVMSWV 59
DB 1 MKYLLPTAAAGLLLLAAQAPMAAEVOLVESGGVVRPGSLRLSCAASGFTDDYGVMSWV 60

QY 60 RQAPKGLWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCA 119
DB 61 RQPPKGLWMI-GYIYSGTYYNPSLKSRTVMSVDTSKNQPSLKLSSVTAVDVAIYYCA 119

QY 120 RMRAPVI-WGGQTLTVTSRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 178
DB 120 RFHPRVVDWGGQTLTVTSRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 179

QY 179 RSYVASWYQKPGQAPVLIYVKNNRPSGIPDRFSGSSGNTASITITGAQAEADYYC 238
DB 180 RSYVASWYQKPGQAPVLIYVKNNRPSGIPDRFSGSSGNTASITITGAQAEADYYC 239

QY 239 NSRDSGNNHVVFGGTTKLTVLGAAAEQKLISEEDLNGAA 277
DB 240 NSRDSGNNHVVFGGTTKLTVLGAAAEQKLISEEDLNGAA 278

RESULT 5

US-09-079-029-11
Sequence 11, Application US/09079029
Patent No. 6342369
GENERAL INFORMATION:
APPLICANT: Adams, Camilla W.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Chundharapal, Anan
APPLICANT: Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids

TYPE: Amino Acid
TOPOLOGY: Linear
US-09-079-029-11

Query Match 67.6%; Score 973; DB 2; Length 310;
Best Local Similarity 71.9%; Pred. NO. 3.7e-71;
Matches 200; Conservative 19; Mismatches 43; Indels 16; Gaps 4;

QY 16 AAQAPMAAEVOLVESGGVVRPGSLRLSCAASGFTDDYGNWSVROAPGKLEWVSGINW 75
DB 33 AAQAPMAAEVOLVESGGVVRPGSLRLSCAASGFTDDYGNWSVROAPGKLEWVSGINW 92

QY 76 NGSSTGYADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARMRAPV---IWGGQTL 132
DB 93 DGGNKYYADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARMRAPV---IWGGQTL 152

QY 133 VTVSRGG 188
DB 153 VTVSRGG 212

QY 189 KPGQAPVLIYVKNNRPSGIPDRFSGSSGNTASITITGAQAEADYYCNSRDSGNNH 248
DB 213 LPGTAPKLLIYDSSNRPSGIPDRFSGSSGNTASITITGAQAEADYYCNSRDSGNNH 272

QY 249 VFGGTTKLTVLGA-----AAEQKLISEEDLNGAA 277
DB 273 VFGGTTKLTVLGA-----AAEQKLISEEDLNGAA 310

RESULT 6

US-09-818-247-22
Sequence 22, Application US/09818247
Patent No. 6855810
GENERAL INFORMATION:
APPLICANT: Mostov, Keith E.
APPLICANT: Chapin, Steven J.
APPLICANT: Richman-Eisenstat, Janice
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Ligands Directed to the No. 6855810-Secretory Component,
TITLE OF INVENTION: No. 6855810-Stalk Region of p19R and Methods of Use Thereof
FILE REFERENCE: 18062E-000910US
CURRENT APPLICATION NUMBER: US/09/818,247
CURRENT FILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-03-27
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22
LENGTH: 288
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial
OTHER INFORMATION: Sequence: Pelb/4AF/myc/6HIS
US-09-818-247-22

Query Match 66.8%; Score 961.5; DB 2; Length 288;
Best Local Similarity 69.4%; Pred. NO. 2.9e-70;
Matches 197; Conservative 26; Mismatches 52; Indels 9; Gaps 4;

QY 1 MKYLLPTAAAGLLLLAAQAPMAAEVOLVESGGVVRPGSLRLSCAASGFTDDYGVMSWVR 60
DB 1 MKYLLPTAAAGLLLLAAQAPMAAEVOLVESGGVVRPGSLRLSCAASGFTDDYGVMSWVR 60

QY 61 QAPKGLWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCAR 120
DB 61 QAPKGLWVSAISGSGSTYADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCAR 120

QY 121 MRAP-----VIWGGQTLTVTSRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 173

Db 241 VQAEGLAVYC--QNDYTPFTFGGKLEI---KREQKISEEDLN 282
||||| ||| ||| :: ||||| : ||||| |||||

RESULT 9

US-09-976-118-1
; Sequence 1, Application US/09976118
; Patent No. 6699473
; GENERAL INFORMATION:
; APPLICANT: Raiesch, Kevin Paul
; APPLICANT: Curiel, David T.
; APPLICANT: Bonner, James Allen
; TITLE OF INVENTION: Human Anti-Epidermal Growth Factor Receptor
; TITLE OF INVENTION: Single-Chain Antibodies
; FILE REFERENCE: D6355
; CURRENT APPLICATION NUMBER: US/09/976,118
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/240,353
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 268
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURES:
; OTHER INFORMATION: amino acid sequence of anti-EGFR scFV
; OTHER INFORMATION: clone pSEX81-6
US-09-976-118-1

Query Match 57.1%; Score 822; DB 2; Length 268;
Best Local Similarity 67.3%; Pred. No. 5.4e-59;
Matches 169; Conservative 21; Mismatches 47; Indels 14; Gaps 3;
Qy 23 EVQLVESGGGVVRRPGGSLRLSCAASGFTFDYDGMWVRQAPGKGLVWVSGINMNGSGTGY 82
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMWVRQAPGKGLVWVSAISSGGSTYY 60
Qy 83 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVTYCARMRAPV-----IWGGTGLV 133
Db 61 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVTYCARMRAPV-----IWGGTGLV 120
Qy 134 TVSRGGGS-----GGGSGGGGSELQDPAPVSLGQVTRITCGDSLRSYASWYQOK 189
Db 121 TVSSGSASAPKLEGEFSEARVQSVLTQPPSLVSPGQTASITCGDKLGDKYASWYQOK 180
Qy 190 PGQAPLVIVYKNNRPSGIPDRFSGSSGNTASLTITGAQAEADYYCNSRDSGNHVV 249
Db 181 PGQSPVLIVYQDKRPSGIPDRFSGSSGNTATLTISGQAWDEADYYCQAWDSSTPY-V 239
Qy 250 FGGGTGLTVLG 260
Db 240 FGTGTVTLG 250

RESULT 10

US-09-192-854-2
; Sequence 2, Application US/09192854
; Patent No. 6696245
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-192-854-2

Query Match 55.8%; Score 803; DB 2; Length 240;
Best Local Similarity 66.2%; Pred. No. 1.6e-57;
Matches 159; Conservative 27; Mismatches 48; Indels 6; Gaps 4;
Qy 23 EVQLVESGGGVVRRPGGSLRLSCAASGFTFDYDGMWVRQAPGKGLVWVSGINMNGSGTGY 82
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMWVRQAPGKGLVWVSAISSGGSTYY 60
Qy 83 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVTYCARMRAPV--IWGGTGLTVTSRGGG 141
Db 61 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVTYCAKSYGAFDYWGQGLTVTVSSGGG 120
Qy 142 SGGSGGGGGSS--ELTQDP-AVSVALGQVTRITCGDSLRSYASWYQOKPGAPVLVI 198
Db 121 SGGSGGGGGSTDIQMTQSPSSLSASVGRVITTCRASQSISSYLNWYQOKPGAPKLLI 180
Qy 199 YGKNNRPSGIPDRFSGSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGQTKLTV 258
Db 181 YAASSLQSGVPSRFGSGSGTDFLTITSSLPEDFATYCCQSYSTPN--TFGGQTKVEI 238

RESULT 11

US-09-511-939-2
; Sequence 2, Application US/09511939
; Patent No. 6846634
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1070
; CURRENT APPLICATION NUMBER: US/09/511,939
; CURRENT FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 2
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-511-939-2

Query Match 55.8%; Score 803; DB 2; Length 240;
Best Local Similarity 66.2%; Pred. No. 1.6e-57;
Matches 159; Conservative 27; Mismatches 48; Indels 6; Gaps 4;
Qy 23 EVQLVESGGGVVRRPGGSLRLSCAASGFTFDYDGMWVRQAPGKGLVWVSGINMNGSGTGY 82
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMWVRQAPGKGLVWVSAISSGGSTYY 60
Qy 83 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVTYCARMRAPV--IWGGTGLTVTSRGGG 141
Db 61 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVTYCAKSYGAFDYWGQGLTVTVSSGGG 120
Qy 142 SGGSGGGGGSS--ELTQDP-AVSVALGQVTRITCGDSLRSYASWYQOKPGAPVLVI 198
Db 121 SGGSGGGGGSTDIQMTQSPSSLSASVGRVITTCRASQSISSYLNWYQOKPGAPKLLI 180
Qy 199 YGKNNRPSGIPDRFSGSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGQTKLTV 258
Db 181 YAASSLQSGVPSRFGSGSGTDFLTITSSLPEDFATYCCQSYSTPN--TFGGQTKVEI 238

RESULT 12

US-09-184-658-63

```
; Sequence 63, Application US/09184658
; Patent No. 6030792
; GENERAL INFORMATION:
; APPLICANT: Otterness, Ivan G.
; APPLICANT: Mezes, Peter S.
; APPLICANT: Mezes, Peter S.
; APPLICANT: Downs, James T.
; APPLICANT: Johnson, Kimberly S.
; TITLE OF INVENTION: Assays for Measurement of Protein Fragments in
; FILE REFERENCE: PC9946-A
; CURRENT APPLICATION NUMBER: US/09/184,658
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/065,423
; EARLIER FILING DATE: 1997-11-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 5109 VH - VL
; OTHER INFORMATION: scFv.
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(22)
; OTHER INFORMATION: pCANTAB6 signal peptide; Val at position 1 is most
; OTHER INFORMATION: likely initiator Met.
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (23)..(138)
; OTHER INFORMATION: 5109 VH domain.
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (139)..(154)
; OTHER INFORMATION: 16 amino acid linker.
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (155)..(266)
; OTHER INFORMATION: 5109 VL domain.
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (270)..(279)
; OTHER INFORMATION: myc tag.
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (284)..(289)
; OTHER INFORMATION: His tag.
; US-09-184-658-63

Query Match          55.6%; Score 800; DB 2; Length 289;
Best Local Similarity 60.3%; Pred. No. 3.6e-57;
Matches 175; Conservative 28; Mismatches 67; Indels 20; Gaps 8;

QY      1 MKYLLPTAAAGLLLLAAQPAEAQVQLVESGQVRRPGSLRLSCAASGFTFDYGMWVR 60
DB      1 MKKLLFAIPLVPPFYAAQPAEAQVQLVESGQVRRPGSLRLSCAASGFTFDYGMWVR 60

QY      61 QAPKGLEWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQNNLSRAEDTAVYYCAR 120
DB      61 QTPDKRLWVATINSNGLTFYADSVKGRFTISRDNKNTLYLQNNLSKSGDSGMYYCVR 120

QY      121 MRAPVI-WGGQTLVTVSRGGGGGGGGSSSE--LTQDP-AVSVALGQTVRITCQ-- 174
DB      121 GYSNYARWGGQALVTVSSGGGGGGGGSDVVMTQTPLTSLVITIGQSASISCKSS 180

QY      175 -----GDSLSRYASWYQKPGQAPVLVIYKNNRPSGIPDRFSGSSSGNTASITITGAQ 229
DB      181 QSLIGSDGLT--YLIWLLQRPQSPKRLIFLVSELDGVPDRFTGSGSGDFTLKISRAE 238

QY      230 ABEADYYCNSRDSGNHV---VFGGGTKLTVLGAABQKLISEEDLNAA 277
DB      239 AEDLGVIYC-----CQGFHFFHTFGAGTKLE-LKAAAEQKLISEEDLNAA 283
```

```
RESULT 13
US-09-504-262D-63
; Sequence 63, Application US/09504262D
; Patent No. 6642007
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Saltarelli, Mary J.
; APPLICANT: Johnson, Kimberly S.
; APPLICANT: Otterness, Ivan G.
; TITLE OF INVENTION: Assays for Measurement of Type II Collagen Fragments in Urine
; FILE REFERENCE: PC10189GPR - CIP of PC9946A
; CURRENT APPLICATION NUMBER: US/09/504,262D
; CURRENT FILING DATE: 2000-02-15
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5109 scFv from clone p5109C scFv7
; OTHER INFORMATION:
; NAME/KEY: misc feature
; OTHER INFORMATION: Description of Artificial Sequence: 5109 VH - VL scFv.
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(22)
; OTHER INFORMATION: pCANTAB6 signal peptide; Val at position 1 is most likely initiat
; OTHER INFORMATION: Or Met.
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (23)..(138)
; OTHER INFORMATION: 5109 VH domain.
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (139)..(154)
; OTHER INFORMATION: 16 amino acid linker.
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (155)..(266)
; OTHER INFORMATION: 5109 VL domain.
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (270)..(279)
; OTHER INFORMATION: myc tag.
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (284)..(289)
; OTHER INFORMATION: His tag.
; US-09-504-262D-63
```

```
Query Match          55.6%; Score 800; DB 2; Length 289;
Best Local Similarity 60.3%; Pred. No. 3.6e-57;
Matches 175; Conservative 28; Mismatches 67; Indels 20; Gaps 8;

QY      1 MKYLLPTAAAGLLLLAAQPAEAQVQLVESGQVRRPGSLRLSCAASGFTFDYGMWVR 60
DB      1 MKKLLFAIPLVPPFYAAQPAEAQVQLVESGQVRRPGSLRLSCAASGFTFDYGMWVR 60

QY      61 QAPKGLEWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQNNLSRAEDTAVYYCAR 120
DB      61 QTPDKRLWVATINSNGLTFYADSVKGRFTISRDNKNTLYLQNNLSKSGDSGMYYCVR 120

QY      121 MRAPVI-WGGQTLVTVSRGGGGGGGGSSSE--LTQDP-AVSVALGQTVRITCQ-- 174
DB      121 GYSNYARWGGQALVTVSSGGGGGGGGSDVVMTQTPLTSLVITIGQSASISCKSS 180

QY      175 -----GDSLSRYASWYQKPGQAPVLVIYKNNRPSGIPDRFSGSSSGNTASITITGAQ 229
DB      181 QSLIGSDGLT--YLIWLLQRPQSPKRLIFLVSELDGVPDRFTGSGSGDFTLKISRAE 238
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Result No.	Query			ID	Description	
	Score	Match	Length			
1	1440	100.0	277	15	US-10-032-037B-25	Sequence 25, Appl
2	1440	100.0	277	15	US-10-029-988B-25	Sequence 25, Appl
3	1440	100.0	277	15	US-10-032-423A-25	Sequence 25, Appl
4	1440	100.0	277	15	US-10-029-926B-25	Sequence 25, Appl
5	1416	98.3	277	15	US-10-032-037B-203	Sequence 203, Appl
6	1416	98.3	277	15	US-10-029-988B-203	Sequence 203, Appl
7	1416	98.3	277	15	US-10-032-423A-203	Sequence 203, Appl
8	1416	98.3	277	15	US-10-029-926B-203	Sequence 203, Appl
9	1388.5	96.4	280	17	US-10-880-922-6	Sequence 6, Appl
10	1379.5	95.8	280	17	US-10-880-922-5	Sequence 5, Appl
11	1379.5	95.8	280	17	US-10-880-922-56	Sequence 56, Appl
12	1378.5	95.7	280	17	US-10-880-922-60	Sequence 60, Appl
13	1378	95.7	266	15	US-10-032-037B-204	Sequence 204, Appl

RESULT 5
US-10-032-037B-203
; Sequence 203, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-203

Query Match 98.3%; Score 1416; DB 15; Length 277;
Best Local Similarity 98.2%; Pred. No. 2.6e-88;
Matches 272; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MKYLLPTAAAGLLLLAAQPMARVQLVSGGGVVRPGGSLRLSCAASGFTFDDYGMWVR 60
Db 1 MKYLLPTAAAGLLLLAAQPMARVQLVSGGGVVRPGGSLRLSCAASGFTFDDYGMWVR 60
Qy 61 QAPKGLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQWNSLRAEDTAVYYCAR 120
Db 61 QAPKGLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQWNSLRAEDTAVYYCAR 120
Qy 121 MRAPVINGQGTLVTVSRGGSGGGGGSSSLTQDPAVSVAGTQVTRITCGDSLRS 180
Db 121 LTHPYFWGQGTLVTVSRGGSGGGGGSSSLTQDPAVSVAGTQVTRITCGDSLRS 180
Qy 181 YASWYQKQKQAPVLVIYGNKRRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNS 240
Db 181 YASWYQKQKQAPVLVIYGNKRRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNS 240
Qy 241 RDSSGNHVFGGKTLTVLGAARAEQKLISEEDLNGAA 277
Db 241 RDSSGNHVFGGKTLTVLGAARAEQKLISEEDLNGAA 277

RESULT 6
US-10-029-988B-203
; Sequence 203, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-203

Query Match 98.3%; Score 1416; DB 15; Length 277;
Best Local Similarity 98.2%; Pred. No. 2.6e-88;
Matches 272; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MKYLLPTAAAGLLLLAAQPMARVQLVSGGGVVRPGGSLRLSCAASGFTFDDYGMWVR 60

Db 1 MKYLLPTAAAGLLLLAAQPMARVQLVSGGGVVRPGGSLRLSCAASGFTFDDYGMWVR 60
Qy 61 QAPKGLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQWNSLRAEDTAVYYCAR 120
Db 61 QAPKGLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQWNSLRAEDTAVYYCAR 120
Qy 121 MRAPVINGQGTLVTVSRGGSGGGGGSSSLTQDPAVSVAGTQVTRITCGDSLRS 180
Db 121 LTHPYFWGQGTLVTVSRGGSGGGGGSSSLTQDPAVSVAGTQVTRITCGDSLRS 180
Qy 181 YASWYQKQKQAPVLVIYGNKRRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNS 240
Db 181 YASWYQKQKQAPVLVIYGNKRRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNS 240
Qy 241 RDSSGNHVFGGKTLTVLGAARAEQKLISEEDLNGAA 277
Db 241 RDSSGNHVFGGKTLTVLGAARAEQKLISEEDLNGAA 277

RESULT 7
US-10-032-423A-203
; Sequence 203, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-203

Query Match 98.3%; Score 1416; DB 15; Length 277;
Best Local Similarity 98.2%; Pred. No. 2.6e-88;
Matches 272; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MKYLLPTAAAGLLLLAAQPMARVQLVSGGGVVRPGGSLRLSCAASGFTFDDYGMWVR 60
Db 1 MKYLLPTAAAGLLLLAAQPMARVQLVSGGGVVRPGGSLRLSCAASGFTFDDYGMWVR 60
Qy 61 QAPKGLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQWNSLRAEDTAVYYCAR 120
Db 61 QAPKGLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQWNSLRAEDTAVYYCAR 120
Qy 121 MRAPVINGQGTLVTVSRGGSGGGGGSSSLTQDPAVSVAGTQVTRITCGDSLRS 180
Db 121 LTHPYFWGQGTLVTVSRGGSGGGGGSSSLTQDPAVSVAGTQVTRITCGDSLRS 180
Qy 181 YASWYQKQKQAPVLVIYGNKRRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNS 240
Db 181 YASWYQKQKQAPVLVIYGNKRRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNS 240
Qy 241 RDSSGNHVFGGKTLTVLGAARAEQKLISEEDLNGAA 277
Db 241 RDSSGNHVFGGKTLTVLGAARAEQKLISEEDLNGAA 277

RESULT 8
US-10-029-926B-203
; Sequence 203, Application US/10029926B
; Publication No. US20040007301A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY

RESULT 11

US-10-880-922-56
; Sequence 56, Application US/10880922
; Publication No. US20050069955A1
; GENERAL INFORMATION:
; APPLICANT: PLAKSIN, DANIEL
; APPLICANT: LEVANON, AVIGDOR
; APPLICANT: SZANTON, ESTHER
; APPLICANT: HAGAY, YOCHVED
; APPLICANT: BEN-LEVY, RACHEL
; APPLICANT: NISGAV, YABL
; APPLICANT: KANFI, YARIV
; TITLE OF INVENTION: ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 10793-143
; CURRENT APPLICATION NUMBER: US/10/880,922
; CURRENT FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/484,061
; PRIOR FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 56
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: consensu antibody
US-10-880-922-56

Query Match 95.8%; Score 1379.5; DB 17; Length 280;
Best Local Similarity 95.7%; Pred. No. 7.7e-86;
Matches 268; Conservative 2; Mismatches 7; Indels 3; Gaps 1;

Qy	1	MKYLLPTAAAGLLLLAAQPAWAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDLNPVKYKH	57
Db	1	MKYLLPTAAAGLLLLAAQPAWAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDLNPVKYKH	60
Qy	58	WVRQAPGKLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYY	117
Db	61	WVRQAPGKLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYY	120
Qy	118	CARMRAPVWGQGLTVTVSRGGSGGGGGSSSELTDPAVSVVALGQTVRITCGDS	177
Db	121	CARLRPPFLWGQGLTVTVSRGGSGGGGGSSSELTDPAVSVVALGQTVRITCGDS	180
Qy	178	LRSYASWYQOKPGQAPVLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYY	237
Db	181	LRSYASWYQOKPGQAPVLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYY	240
Qy	238	CNSRDSGNHVVFGGGLTVLGAAAEQKLISEEDLNGAA	277
Db	241	CNSRDSGNHVVFGGGLTVLGAAAEQKLISEEDLNGAA	280

RESULT 12

US-10-880-922-60
; Sequence 60, Application US/10880922
; Publication No. US20050069955A1
; GENERAL INFORMATION:
; APPLICANT: PLAKSIN, DANIEL
; APPLICANT: LEVANON, AVIGDOR
; APPLICANT: SZANTON, ESTHER
; APPLICANT: HAGAY, YOCHVED
; APPLICANT: BEN-LEVY, RACHEL
; APPLICANT: NISGAV, YABL
; APPLICANT: KANFI, YARIV
; TITLE OF INVENTION: ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 10793-143
; CURRENT APPLICATION NUMBER: US/10/880,922
; CURRENT FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/484,061
; PRIOR FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 60
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: consensu antibody
US-10-880-922-60

Query Match 95.7%; Score 1378.5; DB 17; Length 280;
Best Local Similarity 95.7%; Pred. No. 9e-86;
Matches 268; Conservative 2; Mismatches 7; Indels 3; Gaps 1;

Qy	1	MKYLLPTAAAGLLLLAAQPAWAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDLNPVKYKH	57
Db	1	MKYLLPTAAAGLLLLAAQPAWAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDLNPVKYKH	60
Qy	58	WVRQAPGKLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYY	117
Db	61	WVRQAPGKLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYY	120
Qy	118	CARMRAPVWGQGLTVTVSRGGSGGGGGSSSELTDPAVSVVALGQTVRITCGDS	177
Db	121	CARLRPPFLWGQGLTVTVSRGGSGGGGGSSSELTDPAVSVVALGQTVRITCGDS	180
Qy	178	LRSYASWYQOKPGQAPVLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYY	237
Db	181	LRSYASWYQOKPGQAPVLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYY	240
Qy	238	CNSRDSGNHVVFGGGLTVLGAAAEQKLISEEDLNGAA	277
Db	241	CNSRDSGNHVVFGGGLTVLGAAAEQKLISEEDLNGAA	280

RESULT 13

US-10-032-037B-204
; Sequence 204, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 204
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-204

Query Match 95.7%; Score 1378; DB 15; Length 266;
Best Local Similarity 99.2%; Pred. No. 9.3e-86;
Matches 264; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MKYLLPTAAAGLLLLAAQPAWAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDYGMMSVVR	60
Db	1	MKYLLPTAAAGLLLLAAQPAWAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDYGMMSVVR	60
Qy	61	QAPGKLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCAR	120
Db	61	QAPGKLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCAR	120
Qy	121	MRAPVWGQGLTVTVSRGGSGGGGGSSSELTDPAVSVVALGQTVRITCGDSLRS	180
Db	121	MRAPVWGQGLTVTVSRGGSGGGGGSSSELTDPAVSVVALGQTVRITCGDSLRS	180
Qy	181	YASWYQOKPGQAPVLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNS	240

Db 181 YYASWYQKPGQAPVLVIYGNRRPSGIPDRFGSSSGNTASLTITGAQAEADYYCNS 240
Qy 241 RDSSGNHVFGGKTLTVLGAARQK 266
Db 241 RDSSGNHVFGGKTLTVLGAARQK 266

RESULT 14
US-10-029-988B-204
; Sequence 204, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 204
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-204

Query Match 95.7%; Score 1378; DB 15; Length 266;
Best Local Similarity 99.2%; Pred. No. 9.3e-86;
Matches 264; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKYLLPTAAAGLLLLAAQAPMAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDDYGMWVR 60
Db 1 MKYLLPTAAAGLLLLAAQAPMAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDDYGMWVR 60

Qy 61 QAPKGLEWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAR 120
Db 61 QAPKGLEWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAR 120

Qy 121 MRAPVIMGGTTLVTVSRRGGGGGGGGSSSLTQDPAVSVALGQTIVRITCGDLSRS 180
Db 121 MRAPVIMGGTTLVTVSRRGGGGGGGGSSSLTQDPAVSVALGQTIVRITCGDLSRS 180

Qy 181 YYASWYQKPGQAPVLVIYGNRRPSGIPDRFGSSSGNTASLTITGAQAEADYYCNS 240
Db 181 YYASWYQKPGQAPVLVIYGNRRPSGIPDRFGSSSGNTASLTITGAQAEADYYCNS 240

Qy 241 RDSSGNHVFGGKTLTVLGAARQK 266
Db 241 RDSSGNHVFGGKTLTVLGAARQK 266

RESULT 15
US-10-032-423A-204
; Sequence 204, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 204
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-032-423A-204

Query Match 95.7%; Score 1378; DB 15; Length 266;
Best Local Similarity 99.2%; Pred. No. 9.3e-86;
Matches 264; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKYLLPTAAAGLLLLAAQAPMAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDDYGMWVR 60
Db 1 MKYLLPTAAAGLLLLAAQAPMAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDDYGMWVR 60

Qy 61 QAPKGLEWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAR 120
Db 61 QAPKGLEWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAR 120

Qy 121 MRAPVIMGGTTLVTVSRRGGGGGGGGSSSLTQDPAVSVALGQTIVRITCGDLSRS 180
Db 121 MRAPVIMGGTTLVTVSRRGGGGGGGGSSSLTQDPAVSVALGQTIVRITCGDLSRS 180

Qy 181 YYASWYQKPGQAPVLVIYGNRRPSGIPDRFGSSSGNTASLTITGAQAEADYYCNS 240
Db 181 YYASWYQKPGQAPVLVIYGNRRPSGIPDRFGSSSGNTASLTITGAQAEADYYCNS 240

Qy 241 RDSSGNHVFGGKTLTVLGAARQK 266
Db 241 RDSSGNHVFGGKTLTVLGAARQK 266

Search completed: April 25, 2005, 21:09:47
Job time : 122.531 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 18, 2005, 21:47:37 ; Search time 123.208 Seconds
(without alignments)
939.375 Million cell updates/sec

Title: US-10-029-926D-25

Perfect score: 1440

Sequence: 1 MKYLLPTAAAGLLLLAAQPA.....VLGAARQKLSIEDLNGAA 277

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1440	100.0	277	4	US-10-032-037B-25
2	1440	100.0	277	4	US-10-029-988B-25
3	1440	100.0	277	4	US-10-032-423A-25
4	1440	100.0	277	4	US-10-029-926B-25
5	1436	99.7	277	4	US-10-610-843B-1
6	1416	98.3	277	4	US-10-032-037B-203
7	1416	98.3	277	4	US-10-029-988B-203
8	1416	98.3	277	4	US-10-032-423A-203
9	1416	98.3	277	4	US-10-029-926B-203
10	1397.5	97.0	278	4	US-10-610-843B-2
11	1393.5	96.8	280	4	US-10-611-588C-1
12	1388.5	96.4	280	5	US-10-880-922-6
13	1386.5	96.3	280	4	US-10-610-843B-3
14	1379.5	95.8	280	5	US-10-880-922-5
15	1379.5	95.8	280	5	US-10-880-922-56
16	1378.5	95.7	280	5	US-10-880-922-60
17	1378	95.7	266	4	US-10-032-037B-204
18	1378	95.7	266	4	US-10-029-988B-204
19	1378	95.7	266	4	US-10-032-423A-204
20	1375.5	95.5	280	5	US-10-880-922-61
21	1374.5	95.5	280	5	US-10-880-922-55
22	1294	89.9	291	4	US-10-406-830-6
23	1275.5	88.6	309	4	US-10-052-798-9
24	1275.5	88.6	309	4	US-10-288-917-9
25	1275.5	88.6	309	4	US-10-423-448-9
26	1218.5	84.6	239	3	US-09-880-748-937
27	1218.5	84.6	239	4	US-10-293-418-937

28 1212.5 84.2 239 3 US-09-880-748-2038
29 1212.5 84.2 239 4 US-10-293-418-2038
30 1201.5 83.4 290 3 US-09-969-748C-2
31 1201.5 83.4 290 3 US-09-949-039-2
32 1201.5 83.4 290 5 US-10-470-987-42
33 1194 82.9 312 4 US-10-052-798-10
34 1194 82.9 312 4 US-10-288-917-10
35 1194 82.9 312 4 US-10-423-448-10
36 1191.5 82.7 239 3 US-09-880-748-2015
37 1191.5 82.7 239 3 US-10-293-418-2015
38 1188.5 82.5 296 3 US-09-969-748C-12
39 1188.5 82.5 296 3 US-09-949-039-75
40 1178 81.8 244 4 US-10-322-673-42
41 1178 81.8 244 5 US-10-981-465-42
42 1178 81.8 244 5 US-10-981-465-42
43 1178 81.8 244 5 US-10-981-673-42
44 1178 81.8 244 5 US-10-981-673-42
45 1149 79.8 242 6 US-11-017-030-28

ALIGNMENTS

RESULT 1

US-10-032-037B-25
; Sequence 25, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-25

Query Match 100.0%; Score 1440; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 8e-90;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKYLLPTAAAGLLLLAAQPAEAQVQLVSGGVRPGGSLRLSCAASGFTDDYGMWVR 60
Db 1 MKYLLPTAAAGLLLLAAQPAEAQVQLVSGGVRPGGSLRLSCAASGFTDDYGMWVR 60
Qy 61 QAPFGKLEWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCAR 120
Db 61 QAPFGKLEWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCAR 120
Qy 121 MRAPVWVGQTLVTVSRGGSGGGSGGSELTPDPAVSVALGQTVITCOGDSLRS 180
Db 121 MRAPVWVGQTLVTVSRGGSGGGSGGSELTPDPAVSVALGQTVITCOGDSLRS 180
Qy 181 YYASWYQKQPGQAPLVLYGKNNRPSGIPDRFGSSSGNTASLTITCAQAEDEADYYCNS 240
Db 181 YYASWYQKQPGQAPLVLYGKNNRPSGIPDRFGSSSGNTASLTITCAQAEDEADYYCNS 240
Qy 241 RDSSGNHVPFGGQTKLTVLGAAAEQKLSIEDLNGAA 277
Db 241 RDSSGNHVPFGGQTKLTVLGAAAEQKLSIEDLNGAA 277
RESULT 2
US-10-029-988B-25
; Sequence 25, Application US/10029988B
; Publication No. US20040001839A1

RESULT 4

```

US-10-029-926B-25
; Sequence 25, Application US/10029936B
; Publication No. US20040073011A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277

```

Qy	61	QAPKGLWYSGINWNGGSTGYADSVKGRFTISRDNAKNSLYLQMNSLRABDTAVYICAR	120
Db	61	QAPKGLWYSGINWNGGSTGYADSVKGRFTISRDNAKNSLYLQMNSLRABDTAVYICAR	120
Qy	121	MRAPVINGQGTLLTVSRGGSGGGGGGSGSELTDPAVSVALGQTVRITCGDLSRS	180
Db	121	MRAPVINGQGTLLTVSRGGSGGGGGGSGSELTDPAVSVALGQTVRITCGDLSRS	180
Qy	181	YYASWYQKPGQAPVLVIYGNKNNRPSGIPDRFSGSSGNTASLTITGQAQAEADYIYCNIS	240
Db	181	YYASWYQKPKQA PVLVIYGNKNNRPSGIPDRFSGSSGNTASLTITGQAQAEADYIYCNIS	240
Qy	241	RDSSGNHVFGGGTKLTVLGAAAEOKLISEEDLNGAA	277
Db	241	RDSSGNHVFGGGTKLTVLGAAAEOKLISEEDLNGAA	277

```

1 sequence 1, Application US/10610843B
2 Publication NO. US20040202665A1
3
4 GENERAL INFORMATION:
5
6 APPLICANT: Lazarovits, et al.
7
8 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPEUTIC TREATMENT
9
10 FILE REFERENCE: 10793/72
11
12 CURRENT APPLICATION NUMBER: US/10/610,843B
13
14 CURRENT FILING DATE: 2003-06-30
15
16 PRIOR APPLICATION NUMBER: 60/393,453
17
18 PRIOR FILING DATE: 2002-07-01
19
20 NUMBER OF SEQ ID NOS: 8

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Best Local Similarity	98.2%;	Pred. No. 3.4e-88;							
Matches	272;	Conservative	1;	Mismatches	4;	Indels	0;	Gaps	0;
Qy	1	MKYLLPAAAGLLLLAAQPA	MAEVLQV	ESGGGVVR	PGSRLSL	SCAASGFTDD	DDYGM	SVR	60
Db	1	MKYLLPAAAGLLLLAAQPA	MAEVLQV	ESGGGVVR	PGSRLSL	SCAASGFTDD	DDYGM	SVR	60
Qy	61	QAPKGLIEWSGINWNGSGT	GYADSVKGR	PTISR	DNAKNSLYLQ	NSLRAEDTAV	YVCAR	120	
Db	61	QAPKGLIEWSGINWNGSGT	GYADSVKGR	PTISR	DNAKNSLYLQ	NSLRAEDTAV	YVCAR	120	
Qy	121	MRAPVIMWGQTLVTVSR	GGGGGGGGGGSS	ELTQDPA	VSVALGQTV	VRITCGD	SLRS	180	
Db	121	LTPHYFWGQGLVTVSR	GGGGGGGGGGSS	ELTQDPA	VSVALGQTV	VRITCGD	SLRS	180	
Qy	181	YYASWYQQKPGQAPVL	VIYKKNR	PSGIPDR	FGSSSGNTAS	LTITGAQAEDEAD	YYCNS	240	
Db	181	YYASWYQQKPGQAPVL	VIYKKNR	PSGIPDR	FGSSSGNTAS	LTITGAQAEDEAD	YYCNS	240	
Qy	241	RDSGNHVFPGGG	TKLTVL	GAABEQKLI	SBED	LNAA	277		
Db	241	RDSGNHVFPGGG	TKLTVL	GAABEQKLI	SBED	LNAA	277		

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RESULT 9
US-10-029-926B-203
; Sequence 203, Application US/10029926B
; Publication No. US20040073011A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-926B-203

```

Query Match	98.3%	Score 1416	DB 4	Length 277
Best Local Similarity	98.2%	Pred. No. 3.4e-88		
Matches 272	Conservative 1	Mismatches 4	Indels 0	Gaps 0
Qy 1	MKYLLPTAAAGLLLLAAQ	PAMAEVQLVESGGGV	VRPGSRLSLCAA	SGFTPDDYGM
				SVNR 60
Db 1	MKYLLPTAAAGLLLLAAQ	PAMAEVQLVESGGGV	VRPGSRLSLCAA	SGFTPDDYGM
				SVNR 60
Qy 61	QAPKGILEWVG	GINWNGSGTG	YADSVKGRFT	ISRDNAKNSLYL
				OWNSLRAEDT
Db 61	QAPKGILEWVG	GINWNGSGTG	YADSVKGRFT	ISRDNAKNSLYL
				OWNSLRAEDT
Qy 121	MRAPIVIGQGT	LVTVSRGGSGGGG	GGGGSSLTQDPA	VSVALGQTVR
	:	:	:	ITTCGQDS
Db 121	LTHPYFWGQGT	LVTVSRGGSGGGG	GGGGSSLTQDPA	VSVALGQTVR
	:	:	:	ITTCGQDS
Qy 181	YYASWYQKPKQ	QAPVLVIYGNK	NRPSGTPDRFSG	SSSGNTASLT
				ITTCGAQAE
Db 181	YYASWYQKPKQ	QAPVLVIYGNK	NRPSGTPDRFSG	SSSGNTASLT
				ITTCGAQAE
Qy 241	RDSSGNHVFGG	GTKLTVLGA	AAEQKLI	SEEDLNGAA 277
Db 241	RDSSGNHVFGG	GTKLTVLGA	AAEQKLI	SEEDLNGAA 277

RESULT 10
US-10-610-843B-2
; Sequence 2, Application US/10610843B
; Publication No. US20040202665A1


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Db 1 MKYLLPTAAAGLLLLAAQPMABEVQLVESGGGVVRRPGSLRLSCAASGFTFDLNPVKVHM 60
Qy 58 WVRQAPGKLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYY 117
Db 61 WVRQAPGKLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYY 120
Qy 118 CARMRAPIVWGQGTTLVTVSRGGSGGGGGSSSELTQDPAVSVALGQTVRITCGDS 177
Db 121 CARLRPSIWGGGTTLVTVSRGGSGGGGGSSSELTQDPAVSVALGQTVRITCGDS 180
Qy 178 LRSYASWYQKPGQAPVLIYGNKRPISGIPDRFSGSSSGNTASLTITGAQAEDEADYY 237
Db 181 LRSYASWYQKPGQAPVLIYGNKRPISGIPDRFSGSSSGNTASLTITGAQAEDEADYY 240
Qy 238 CNSRDSGNHVFVGGGTKLTVLGAAAEQKLISEEDLNGAA 277
Db 241 CNSRDSGNHVFVGGGTKLTVLGAAAEQKLISEEDLNGAA 280
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RESULT 15

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US-10-880-922-56
; Sequence 56, Application US/10880922
; Publication No. US2005069955A1
; GENERAL INFORMATION:
; APPLICANT: PLAKSIN, DANIEL
; APPLICANT: LEVANON, AVIGDOR
; APPLICANT: SZANTON, ESTHER
; APPLICANT: HAGAY, YOCHAVED
; APPLICANT: BEN-LEVY, RACHEL
; APPLICANT: NISGAV, Yael
; APPLICANT: KANFI, YARIV
; TITLE OF INVENTION: ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 10793-143
; CURRENT APPLICATION NUMBER: US/10/880,922
; CURRENT FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/484,061
; PRIOR FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 56
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Consensus antibody
US-10-880-922-56
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Query Match 95.8%; Score 1379.5; DB 5; Length 280;
Best Local Similarity 95.7%; Pred. No. 1e-85;
Matches 268; Conservative 2; Mismatches 7; Indels 3; Gaps 1;

Qy 1 MKYLLPTAAAGLLLLAAQPMABEVQLVESGGGVVRRPGSLRLSCAASGFTFD---DYGMS 57
Db 1 MKYLLPTAAAGLLLLAAQPMABEVQLVESGGGVVRRPGSLRLSCAASGFTFDLNPVKVHM 60
Qy 58 WVRQAPGKLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYY 117
Db 61 WVRQAPGKLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYY 120
Qy 118 CARMRAPIVWGQGTTLVTVSRGGSGGGGGSSSELTQDPAVSVALGQTVRITCGDS 177
Db 121 CARLRVFLWGQGTTLVTVSRGGSGGGGGSSSELTQDPAVSVALGQTVRITCGDS 180
Qy 178 LRSYASWYQKPGQAPVLIYGNKRPISGIPDRFSGSSSGNTASLTITGAQAEDEADYY 237
Db 181 LRSYASWYQKPGQAPVLIYGNKRPISGIPDRFSGSSSGNTASLTITGAQAEDEADYY 240
Qy 238 CNSRDSGNHVFVGGGTKLTVLGAAAEQKLISEEDLNGAA 277
Db 241 CNSRDSGNHVFVGGGTKLTVLGAAAEQKLISEEDLNGAA 280
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Search completed: November 18, 2005, 22:17:52
Job time : 124.208 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2005, 21:53:49 ; Search time 3.49527 Seconds
(without alignments)
89.536 Million cell updates/sec

Title: US-10-029-926D-25

Perfect score: 1440

Sequence: 1 MKYLLPTAAAGLLLLAQA.....VLGAABEQKLISEDLNGAA 277

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/FCI_NEW_PUB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	719	49.9	625	1	US-10-512-184-47
2	690	47.9	269	1	US-10-839-799-109
3	676.5	47.0	618	1	US-10-512-184-48
4	672	46.7	250	1	US-10-512-184-27
5	672	46.7	327	1	US-10-512-184-62
6	672	46.7	327	1	US-10-512-184-64
7	672	46.7	328	1	US-10-512-184-63
8	672	46.7	576	1	US-10-512-184-65
9	670	46.5	252	1	US-10-512-184-28
10	668.5	46.4	313	1	US-10-512-184-72
11	649.5	45.1	329	1	US-10-512-184-68
12	648	45.0	258	1	US-10-512-184-26
13	644.5	44.8	261	1	US-10-512-184-35
14	641.5	44.5	263	1	US-10-512-184-29
15	638.5	44.3	329	1	US-10-512-184-70
16	629	43.7	320	1	US-10-512-184-67
17	629	43.7	569	1	US-10-512-184-66
18	625.5	43.4	259	1	US-10-512-184-31
19	614.5	42.7	251	1	US-10-512-184-33
20	605	42.0	259	1	US-10-512-184-30
21	604.5	42.0	626	1	US-10-512-184-49
22	604	41.9	543	1	US-10-495-664-3
23	573.5	39.8	317	1	US-10-512-184-69
24	557	38.7	371	1	US-10-512-184-71
25	553	38.4	615	1	US-10-512-184-50

26	549.5	38.2	248	1	US-10-512-184-32
27	533	37.0	259	1	US-10-512-184-34
28	490.5	34.1	444	7	US-11-172-320-6
29	488.5	33.9	122	7	US-11-144-248-24
30	485	33.7	470	7	US-11-144-248-46
31	481.5	33.4	248	1	US-10-512-184-36
32	480	33.3	138	1	US-10-789-273-8
33	479.5	33.3	473	7	US-11-144-248-50
34	478	33.2	121	1	US-10-789-273-9
35	477	33.1	138	1	US-10-789-273-12
36	474	32.9	470	7	US-11-144-248-49
37	469	32.6	125	7	US-11-144-248-16
38	468.5	32.5	139	1	US-10-721-763-33
39	466	32.4	470	7	US-11-144-248-45
40	451	31.3	124	7	US-11-144-248-8
41	446	31.0	98	1	US-10-789-273-10
42	446	31.0	98	7	US-11-144-248-32
43	439	30.5	98	7	US-11-144-248-30
44	423	29.4	121	7	US-11-077-978-2
45	420.5	29.2	120	7	US-11-077-978-7

ALIGNMENTS

RESULT 1

US-10-512-184-47
; Sequence 47, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 625
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: fusion protein
; OTHER INFORMATION: comprising the leader peptide - chitinase - linker
; OTHER INFORMATION: - scfV CWP2 - cmvc/His6.
US-10-512-184-47

Query Match 49.9%; Score 719; DB 1; Length 625;
Best Local Similarity 57.2%; Pred. No. 2e+30;
Matches 162; Conservative 23; Mismatches 68; Indels 30; Gaps 9;

Qy	16	AAQAPAAEVLVSQGGVVRPGGSLRLSCAASGFTPDYGNMWSVRQAPGKLEWVGINW	75
Db	337	AAQAPAAAVTLDSGGGLQTPGGGLSLVCKGSGDFSDTMMWRQAPGKLEFVAGISG	396
Qy	76	NGSGTGVADSVKGFPTISRDNKNSLYLQNSLRRAETATVYTCARMAPV-----	125
Db	397	DGSDTNYGSAVKGRATISRDNQSGSTVRLQLNLRRAETATVYCT--RGPCSPTRKCAADR	454
Qy	126	--TWGQGTTLTVSRGG--GGSGGGGGGG--GSELTQDPAVSVALGOTVTRITCGDSLR	179
Db	455	IDAWGHGTETVVSQSGTSGSGKPGEGSTKGAPALTPQSPVSANILGTVETICSGG---	511
Qy	180	SYASWYQOK-PGQAPVLVIYGNK---NRPSGIPDRFSGSSGNSTASITITGAQAEAD	235
Db	512	GTRYGNFQOKSPGAPVTVIYWDSDSANRPSNIPSRFSGTSGSTATLTITGVQADDEAV	571
Qy	236	YCNRRDSSGNHV-VFGGGTKLTVLG-----AAAEQKLISEDL 273	
Db	572	YFCGSDYRRSGYVIFGAGTTLTVLGQFVDAAAEQKLISEDL 614	

```

RESULT 2
US-10-839-799-109
; Sequence 109, Application US/10839799
; Publication No. US20050249726A1
; GENERAL INFORMATION:
; APPLICANT: OHTOMO, Toshihiko
; SATO, Koh
; TSUCHIYA, Masayuki
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; MEDULLOBLASTOMA CELLS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/839,799
; FILING DATE: 06-May-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,265
; FILING DATE: 09-SEP-1996
; APPLICATION NUMBER: WO PCT/JP94/01763
; FILING DATE: 19-OCT-1994
; APPLICATION NUMBER: JP 5-291078
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/184
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 109:
US-10-839-799-109
Query Match 47.9%; Score 690; DB 1; Length 269;
Best Local Similarity 53.8%; Pred. No. 3.1e-29;
Matches 142; Conservative 39; Mismatches 73; Indels 10; Gaps 5;

Qy 1 MKYLLPTAAGLLLLAAQPMAMAEVLQVSGGVVVRPGGSLRLSCAASGFTFDDYGMSSWR 60
Db 1 MKYLLPTAAGLLLLAAQPMAMAEVLQVSGGVVVRPGGSLRLSCAASGFTFDDYGMSSWR 60
Qy 61 QAPGKGLWYSGINWNGSGTCYADSVKGRFTISRDNAKNSLYLQMSLRSEDYAVYCAR 120
Db 61 QAPGQGLWNGRIDPADGNTKYDPKQGRVTITADESTNTAYMELSLRSEDYAFYFCA- 119
Qy 121 MRAPVI----WGQGLTVTSRGGGGGGGGGGSS-ELTQDP-AVSVALGQTVRITCO 174
Db 120 -SAYVNDYWGQGLTVTSRGGGGGGGGGGSDIQMTQSPSSIASVGDVITCK 178
Qy 175 GDSLSRSYASWYQKPGQAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAE 234
Db 179 ASQNVGTNVAWYQKPGKAPKPLIYASVYSGVPSRFGSGSGTDFTFITSSIQPDIA 238
Qy 235 DYICNSRSDSSGNHVVFQGGTKLTV 258

US-10-512-184-48
; Sequence 48, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Forderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 48
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: fusion protein
; OTHER INFORMATION: comprising the leader peptide - chitinase - linker
; OTHER INFORMATION: - scFv VD2 - cmcy/His6.
US-10-512-184-48
Query Match 47.0%; Score 676.5; DB 1; Length 618;
Best Local Similarity 52.7%; Pred. No. 2.4e-28;
Matches 145; Conservative 38; Mismatches 71; Indels 21; Gaps 8;

Qy 16 AAQPMAMAEVLQVSGGVVVRPGGSLRLSCAASGFTFDDYGMSSWRQAPGKGLWYSGINW 75
Db 337 AAQPMAMAEVLQVSGGVVVRPGGSLRLSCAASGFTFDDYGMSSWRQAPGKGLWYSGINW 396
Qy 76 NGSTGYADSVKGRFTISRDNAKNSLYLQMSLRSEDYAVYCAR-MRAPV-----TWQGG 130
Db 397 YTGATYADSVKGRFTISRDNAKNSLYLQMSLRSEDYAVYCAR-MRAPV-----TWQGG 456
Qy 131 TLVTSRGGGGGGGGGGGGSS-ELTQDP-AVSVALGQTVRITCOG-----SLRSYVA 183
Db 457 TSVTVSAGGGGGGGGGGGGGSDVLTMTQPLSLPVLGDAQSISCRSSQNVHSNGTYL 516
Qy 184 SWYQKPGQAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEADYVYCNRS 243
Db 517 QWYLKPGQSPKLLIYKASNRPSGVPARFSGSGSGTDFTLKISRVAEDLGVIYVC----F 572
Qy 244 SGNHV--VFGGQTKLTV---LGRAAEQKLISEEDL 273
Db 573 QGSHVPTFGGQTKLEIKRAVDAARQKLISEEDL 607

RESULT 4
US-10-512-184-27
; Sequence 27, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Forderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 27
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv SGB3 with

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;
; OTHER INFORMATION: Description of Artificial Sequence: precursor
;
; OTHER INFORMATION: fusion protein comprising MBP - linker -
; OTHER INFORMATION: scFv Plp9.
US-10-512-184-72

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Query Match	46.4%	Score 668.5	DB 1	Length 313
Best Local Similarity	54.7%	Pred. No. 3.8e-28		
Matches 146	Conservative 29	Mismatches 67	Indels 25	Gaps 8

Qy	16	AAOPAMAEVLVESGGGVRRPGGSIRLSCAASGTFDDYGNMSWTRQAPKGLEWVSGINW	75
Db	48	AAOPAMAAVTLDESGGGLQTPGGALSVCASGDFPKGYEMAWTRQAPKGLEWVAAIS-	106
Qy	76	NGSGTYGADSVKGRFTTIRDNAKNSLYLQWNSLRAEDTAVVYCARMAAPV-----	125
Db	107	SGYNTNTYGAAGKGRATTIRNNGQSTFVRLQLNLNRAEDTATVYCAKTHGYGCAGNWC	166
Qy	126	----IMQCGTLVTVSRGG-GSGSGGGSGGG---GSSLTDPAPVSVALGQTVRITCGQDS	177
Db	167	GNIDAWCHGTEVTVSSGSTSGSGKPGPGEGSTKGAPGLTQASSVSANPGETVKTICSGGG	226
Qy	178	--LRSYVASWYQOK-PCGAPVLVIYTKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEA	234
Db	227	SYAGSYYYGWYQKTPGSAPTVIYSNDKRPSPNIPSRFSGSLSGSTNTLTITGTQVQVDEA	286
Qy	235	DYYCNSRDSGSHV-VFGGGTKLTVLG	260
Db	287	YVFCGAYDN--NYAGIFGAGTTLTVLG	311

```

RESULT 11
US-10-512-184-68
; Sequence 68, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: precursor
; OTHER INFORMATION: fusion protein comprising RS - linker scFv VD2.
US-10-512-184-68

```

Query Match	45.1%	Score 649.5;	DB 1;	Length 329;
Best Local Similarity	51.0%;	Pred. No. 3.4e-27;		
Matches 133;	Conservative 43;	Mismatches 70;	Indels 15;	Gaps 6

Qy	16	AAAPAMAEVLVEGGG	VVRPGGSILRLSLCAASGPTFDDY	SGMSVWQAQPKGLEWVGINW	75
		:	: :	: :	:
		:	: :	: :	:
		:	: :	: :	:
Db	66	AAAPAMAEVKLLESGPELK	PGETVKISCKASGYTFTKYGNWVKQA	PKGLKMWGINWT	125
		:	: :	: :	:
		:	: :	: :	:
		:	: :	: :	:
Qy	76	NGSGTGADSVKGRTTISRDN	AKNSLYLOMNSLRABDTATVTTCARMA-	PV-----IWGG	130
		:	: :	: :	:
		:	: :	: :	:
Db	126	YTGETTYADDPKGFAPAFS	LSTSTAPLIQLNNLNEDTATFYCARYYGNPY	TMTDYWGQG	185
		:	: :	: :	:
		:	: :	: :	:
		:	: :	: :	:
Qy	131	TLTVSRGGGGGGGGGGGGSS--ELTDQP--AVSVALGQT	VRITCGDLSRSY-----Y	182	
		:	: :	: :	:
		:	: :	: :	:
Db	186	TSLTVSGGGGGGGGGGGGGSDIVLSQSPSSLVASV	GKEVTMSCSKSQSLLYSSNQNY	245	
		:	: :	: :	:
		:	: :	: :	:
		:	: :	: :	:
Qy	183	ASWTQQRPQGAQPVLVITYGNKNRPPGIIPDRFGSS	SGNNTASTITGAQADEADYYCNSRD	242	
		:	: :	: :	:
		:	: :	: :	:
Db	246	LAWYQQPQSGPSKLIIYWASTRFSGVPDRPTFGSG	SGDTFTLTISVKAEDLAVVYCOOY	305	
		:	: :	: :	:
		:	: :	: :	:
		:	: :	: :	:

Qy 243 SSGNHVFGGTKLTVLGAAA 263
Db 306 S--YPFTFGSGTKLEIKRADA 324

```

RESULT 12
US-10-512-184-26
; Sequence 26, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.v.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 258
; TYPE: PR1
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv CWP2
; OTHER INFORMATION: with specificity against Fusarium spp.; originates
; OTHER INFORMATION: from Gallus gallus.
US-10-512-184-26

```

Query Match	45.0%	Score 648;	DB 1;	Length 258;
Best Local Similarity	55.2%;	Pred. No. 3.4e-27;		
Matches 144;	Conservative 23;	Mismatches 68;	Indels 26;	Gaps 8;

Qy	21	MAEVLVESGGVVRPGGSLRLSCASGFTFDDYGHMSWVRQAPKGLEWYSGINWNGST	80
Db	1	MAAVTLDESGGGLQTPGGGLSLVCKSGGDFPSDPTMMWVRQAPKGLEFVAGISGDGSDT	60
Qy	81	GYADS VKGRTTISRDNAKNSLYIQMSLRAREDYAVVYCARMAPV-----IWG	128
Db	61	NYGSVKGRTATISRDNQSGTVRLQLNLRAREDYATYYCT--RGPCSTPKCAADRIADWG	118
Qy	129	QGLTVTVSRGG-GGSGGGGGGG---GSSBLTQDPAVSVALGQTVRITCQDLSLRSYAS	184
Db	119	HGTEVTVSSGTSGGSKPGGEGSTKGAPALTQPSVSANLGGTVEITCSG---GYRYG	175
Qy	185	WYQOK-PGOAPVLVIYGNK---NRPGCIPDRFGSSSGNTASLTITGAQAEDEADYYCNS	240
Db	176	WFQOKSPGSAPTVIYWDDBSANRPSNI PSRFGSGTSGSTATLTITGVQADDEAVYFCGS	235
Qy	241	RDSSGNHV-VFGGGTKLTVLG	260
Db	236	YDRSSGYVSIFGAGTTLTVLG	256

```

RESULT 13
US-10-512-184-35
; Sequence 35, Application US/10512184
; Publication NO. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Artificial Sequence

```

```
;
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv Plp9 with
; OTHER INFORMATION: specificity against Phoma lingam; originates from
; OTHER INFORMATION: Mus musculus.
US-10-512-184-35

Query Match          44.8%; Score 644.5; DB 1; Length 261;
Best Local Similarity 53.8%; Pred. No. 5.1e-27;
Matches 141; Conservative 29; Mismatches 67; Indels 25; Gaps 8;

Qy 21 MAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDDYGMSSWVRQAPGKLEWVSGINWNGST 80
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1  MAAVTLDESGLGLTQPGALSLSLVCKASGDFPKGYEMAWVRQAPGKLEWVAALS-SCYNT 59
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 81 GYADSVKGRFTISRDNKNSLYLQMSLRADETAIVYICARMRAPV-----I 126
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 60 NYGAAGVGRATISRNQSTVRLQLNLRAEDTATYYCAKTHGYGCAGNWCAGNIDA 119
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 127 WGQGLTLVTSRGG-GGSGGGGGGG-----GSSELTQDPAVSVALGQTVRITCOGDS--LRS 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 120 WGHGTEVTVSSGTSSTGSGKPGGEGSTKGAPGLTQASSVSANPGETVKITCSGGGVSAGS 179
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 181 YYASWYQOK-PGQAPVLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEADYYCN 239
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 180 YYIGWYQKTPGSAPVTVIYNDKRPSPNIPRFSGLSGSTNTLTITGVQVDDNAVYFCG 239
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 240 SRDSSGNHV-VFGGTTKLTVLG 260
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 240 AYDN--NYAGIFAGTTLTVLG 259
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
US-10-512-184-29
; Sequence 29, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Forderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCES: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 29
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: precursor
; OTHER INFORMATION: fusion protein comprising RS - linker - scFv VDM2.
US-10-512-184-70

Query Match          44.3%; Score 638.5; DB 1; Length 329;
Best Local Similarity 50.8%; Pred. No. 1.2e-26;
Matches 132; Conservative 42; Mismatches 72; Indels 15; Gaps 6;

Qy 16 AAQPMARAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDDYGMSSWVRQAPGKLEWVSGINW 75
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 66 AAQPMARAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDDYGMSSWVRQAPGKLEWVSGINW 135
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 76 NGGSTGYADSVKGRFTISRDNKNSLYLQMSLRADETAIVYICARMRA-PV-----IWGQG 130
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 126 YTGEPYVADDFKGRPAFSLSTSTAFQLQNNLNKEDTATYFCARYGNPNPYTMDYWGQG 185
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 131 TLVTVSRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 182
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 186 TSLTVSSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 245
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 183 ASWYQOKPGQAPVLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRD 242
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 246 LAMYQOKPGQSPKLLIYMASTRSGVDPDRFTGSGSGTDFTLTISSVKAEADLAVYICQYY 305
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Query Match          44.5%; Score 641.5; DB 1; Length 263;
Best Local Similarity 53.1%; Pred. No. 7.2e-27;
Matches 138; Conservative 35; Mismatches 68; Indels 19; Gaps 8;

Qy 21 MAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDDYGMSSWVRQAPGKLEWVSGINWNGST 80
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1  MAEVQLVESGGGLVRRPGNSLKLSCVTSFTFSNYRHWLQPPGKRLIEWIAVVKSEN 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 81 G--YADSVKGRFTISRDNKNSLYLQMSLRADETAIVYICARMRA-PV-----IWGQGLTVTS 136
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 GADYAESVKGRFTISRDRDSSRVYLNRLREEDTATYICRSSESSEGGFPYWGQGLTVTS 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 137 RG---GGSGGGGGG-----GGSSSELTQDP-AVSVALGQTVRITCO-CDSL-----RSYYA 183
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 SGSTSGGKPGPGGSGTKGAPDQMTQSPSLSVSAGEKVTLSCKSSQSLNSGNQCNFL 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 184 SWYQOKPGQAPVLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDS 243
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```
Db 181 AWYQOKPGQPPKLLIYGASTRESGVPARFTGSGSGTDFTLTISSVQAEADQAVYICQNDHS 240
Qy 244 SGNHVVFGGTTKLTVLGAAA 263
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 --YPFTFGSGTKLEIKRADA 258
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
US-10-512-184-70
; Sequence 70, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Forderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCES: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 70
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: precursor
; OTHER INFORMATION: fusion protein comprising RS - linker - scFv VDM2.
US-10-512-184-70

Query Match          44.3%; Score 638.5; DB 1; Length 329;
Best Local Similarity 50.8%; Pred. No. 1.2e-26;
Matches 132; Conservative 42; Mismatches 72; Indels 15; Gaps 6;

Qy 16 AAQPMARAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDDYGMSSWVRQAPGKLEWVSGINW 75
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 66 AAQPMARAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDDYGMSSWVRQAPGKLEWVSGINW 135
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 76 NGGSTGYADSVKGRFTISRDNKNSLYLQMSLRADETAIVYICARMRA-PV-----IWGQG 130
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 126 YTGEPYVADDFKGRPAFSLSTSTAFQLQNNLNKEDTATYFCARYGNPNPYTMDYWGQG 185
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 131 TLVTVSRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 182
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 186 TSLTVSSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 245
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 183 ASWYQOKPGQAPVLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRD 242
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 246 LAMYQOKPGQSPKLLIYMASTRSGVDPDRFTGSGSGTDFTLTISSVKAEADLAVYICQYY 305
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Search completed: November 18, 2005, 22:18:07
Job time : 4.49527 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2005, 21:35:01 ; Search time 27.0883 Seconds
(without alignments)
983.894 Million cell updates/sec

Title: US-10-029-926d-25

Perfect score: 1440

Sequence: 1 MKYLLPTAAAGLLLLAAQPA.....VLGHAARQKLISEEDLNGAA 277

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_80:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	643.5	44.7	268	2 A56446	Ig heavy chain V r
2	568	39.4	109	2 S19663	Ig lambda chain V r
3	565.5	39.3	249	2 S41374	single chain Fv an
4	562	39.0	108	2 S47184	Ig lambda chain -
5	551.5	38.3	110	2 S36272	Ig lambda chain V
6	546	37.9	127	2 S70444	Ig lambda chain pr
7	541	37.6	108	2 S38498	Ig lambda chain -
8	539	37.4	109	2 S38496	Ig lambda chain -
9	530.5	36.8	233	2 S25748	Ig lambda chain -
10	527	36.6	108	1 L3HUSH	Ig lambda chain V-
11	522.5	36.3	233	2 J05322	p53 specific singl
12	518.5	36.0	110	2 S19672	Ig lambda chain V
13	518	36.0	146	2 S02083	Ig lambda chain V-
14	513	35.6	98	2 S26928	Ig heavy chain V r
15	510.5	35.5	128	2 S31595	Ig heavy chain V r
16	503	34.9	96	2 S36060	Ig lambda chain -
17	503	34.9	115	2 S13726	Ig lambda chain V
18	503	34.9	121	2 S31118	Ig heavy chain - h
19	502.5	34.9	233	2 S25741	Ig lambda chain -
20	502	34.9	123	2 S30532	Ig heavy chain V r
21	501	34.8	121	2 S31104	Ig heavy chain (su
22	495.5	34.4	112	2 PH1654	Ig heavy chain V r
23	491	34.1	120	2 S36273	Ig heavy chain V r
24	489.5	34.0	145	2 S11239	Ig heavy chain V r
25	489	34.0	134	2 S31699	Ig heavy chain V r
26	488	33.9	138	2 S31666	Ig heavy chain pre
27	486	33.8	160	2 S05271	Ig heavy chain V-D
28	485.5	33.7	120	2 S44111	Ig heavy chain - h
29	485	33.7	119	2 S31108	Ig heavy chain - h

ALIGNMENTS

RESULT 1

A56446

Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/c)

C:Species: Mus musculus (house mouse)

C:Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996

C:Accession: A56446

R:Tang, P.W.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.

J. Biol. Chem. 270, 7829-7835, 1995

A:Title: A high affinity digoxin-binding protein displayed on M13 is functionally identical

A:Reference number: A56446; MUID:95229583; PMID:7713873

A:Accession: A56446

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-268 <TRAN>

A:Cross-references: UNIPARC:UPI000017C6D0; GB:U20617

C:Keywords: heterotetramer; immunoglobulin

Query Match 44.7%; Score 643.5; DB 2; Length 268;

Best Local Similarity 51.3%; Pred. No. 3.4e-36;

Matches 139; Conservative 35; Mismatches 80; Indels 17; Gaps 6;

Qy	21	MAEVQLVESGGGVVPRPGSGSLRLSCAASGFTFDDYGMGWVRQAPGKGLIEWSGINWNGST	80
Db	1	MAQVLQESGAEVLKPGASVKLSCTTSGFNIKDYTHMWVKQRPQGLEWIGRIAPANGIT	60
Qy	81	GYADSVKGRFTISRDNAKNSLYLQMSLRADETAVYYCAR---MRAPVWGQGLTVTVSR	137
Db	61	KYDPKFGQKATIAADTSNTAYLQLSLTSEDYAVYTCASYLTRYENYWGQGLTVTVSS	120
Qy	138	GGGSGGGSGGGGSS-ELTQDPAV-SVALGQTVRITCGDLSRSYASWYQKPGQAPV	195
Db	121	GGGSGGGSGGGGSDIELTQSPAIMSALGEEKYMTSCRASSSYN-FIYWYQKSDASPK	179
Qy	196	LVIYKKNRPSGIDPFGSGSGNNTLTITGAQAEADYVYCNRSRSGNHNWVFGGQTK	255
Db	180	LWVYTHLPFGVPARFSGSGSGNSYSLTSSMEGDAATYYCQQTFS--PFTFGSGTK	237
Qy	256	LTVLGA-----AAEQKLISEEDLNGAA	277
Db	238	LEIKRSAHHHHHHGAAEQKLISEEDLNGAA	268

RESULT 2

S19663

Ig lambda chain V region (clone alpha-BSA3) - human

C:Species: Homo sapiens (man)

C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000

C:Accession: S19663

R:Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,

J. Mol. Biol. 222, 581-597, 1991

A:Title: BY-passing immunization. Human antibodies from V-gene libraries displayed on ph

A:Reference number: S19663; MUID:92085276; PMID:1748994

A/Accession: S19663
A/Molecule type: mRNA
A/Residues: 1-109 <MAR>
A/Cross-references: UNIPARC:UPI0000039C3B; EMBL:X61640; NID:G29492; PIDN:CAA43821.1; PII
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
P/15-89/Domain: immunoglobulin homology <IMM>

Query Match 39.4%; Score 568; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.5e-31;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 152 SSELTPPAVSVALGQTVRITTCGDSLSRSYASWYQKPGQAPVLVIYGNRPSPGIPDR 211
Db 1 SSELTPPAVSVALGQTVRITTCGDSLSRSYASWYQKPGQAPVLVIYGNRPSPGIPDR 60
Qy 212 FSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGKLTVLG 260
Db 61 FSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGKLTVLG 109

RESULT 3
S41374
Ig lambda chain Fv antibody - mouse
C/Species: Mus musculus (house mouse)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C/Accession: S41374
R/Artsenko, O.; Weller, E.W.; Muentz, K.; Conrad, U.
submitted to the EMBL Data Library, January 1994
A/Description: Construction and functional characterization of a single chain Fv antibody
A/Reference number: S41374
A/Accession: S41374
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-249 <ART>
A/Cross-references: UNIPARC:UPI000017C74A; EMBL:Z29480

Query Match 39.3%; Score 565.5; DB 2; Length 249;
Best Local Similarity 48.2%; Pred. No. 5.2e-31;
Matches 123; Conservative 37; Mismatches 74; Indels 21; Gaps 6;

Qy 23 EVLVRSGGGVPPGSGSLRSLCAASGFTFDYGMVSRQAPGKLEWVSGINWNGSTGY 82
Db 1 QVQLQSGAEALVPGASVKLSCTASGTFNFKDDYIHWYKQPEKLEWIAIPASGVKY 60
Qy 83 ADSVKGRFTISRDNKNSLYLQNSLRDAETAVYYCAR----MRAPVWGQGLTVTVSRG 138
Db 61 VPRFQDKATITADTSSNTAYLLLSLTSEDYAVYCARRDYLTSLGYWGQGSTVTVSSR 120
Qy 139 GGGSGGGSGGGSS-ELTQD-PAVSVALGQTVRITCQ-----GDSLSRSYASWYQ 187
Db 121 GGGSGGGSGGGSGSDIELTQSPSPVVPVIGESVSISCRSKSLYSDGDS----YLFWFL 176
Qy 188 QKPGQAPVLVIYGNRPSPGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSSGNH 247
Db 177 QRPGQSPQLLIYRMSNLASGVDRFSGSGSGTFTLIRSRVEADGVYTCMQHRE--YP 234
Qy 248 VVFGGGKLTVLGAA 262
Db 235 LTFGAGTKLKLKRAA 249

RESULT 4
S47184
Ig lambda chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C/Accession: S47184
R/McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
submitted to the EMBL Data Library, June 1994
A/Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patient
A/Reference number: S47181
A/Accession: S47184

A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-108 <NCI>
A/Cross-references: UNIPARC:UPI0000031AP6; EMBL:X79783; NID:G506426; PIDN:CAA56179.1; PII
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
P/15-89/Domain: immunoglobulin homology <IMM>

Query Match 39.0%; Score 562; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.7e-31;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 152 SSELTPPAVSVALGQTVRITTCGDSLSRSYASWYQKPGQAPVLVIYGNRPSPGIPDR 211
Db 1 SSELTPPAVSVALGQTVRITTCGDSLSRSYASWYQKPGQAPVLVIYGNRPSPGIPDR 60
Qy 212 FSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGKLTVL 259
Db 61 FSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGKLTVL 108

RESULT 5
S36272
Ig lambda chain V region (clone alpha-THY-29) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C/Accession: S36272
R/Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.;
EMBO J. 12, 725-734, 1993
A/Title: Human anti-self antibodies with high specificity from phage display libraries.
A/Reference number: S36256; MUID:93178448; PMID:7679990
A/Accession: S36272
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-110 <GRI>
A/Cross-references: UNIPARC:UPI0000118DP6; EMBL:Z18833; NID:G33419; PIDN:CAA79285.1; PII
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
P/15-89/Domain: immunoglobulin homology <IMM>

Query Match 38.3%; Score 551.5; DB 2; Length 110;
Best Local Similarity 98.2%; Pred. No. 1.9e-30;
Matches 108; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 152 SSELTPPAVSVALGQTVRITTCGDSLSRSYASWYQKPGQAPVLVIYGNRPSPGIPDR 211
Db 1 SSELTPPAVSVALGQTVRITTCGDSLSRSYASWYQKPGQAPVLVIYGNRPSPGIPDR 60
Qy 212 FSGSSSGNTASLTITGAQAEADYYCNSRDSSGN-HVVFGGTKLTVLG 260
Db 61 FSGSSSGNTASLTITGAQAEADYYCNSRDSSGNLYVVFGGTKLTVLG 110

RESULT 6
S70444
Ig lambda chain precursor V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 31-Dec-2004
C/Accession: S70444; S70426
R/Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelie, C.
Mol. Immunol. 29, 1363-1373, 1992
A/Title: IgM kappa/lambda Bv human B cell clone: an early step of differentiation of fet
A/Reference number: S70442; MUID:93024508; PMID:1383695
A/Accession: S70444
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-127 <CUI>
A/Cross-references: UNIPROT:QNSD6; UNIPARC:UPI0000176807
A/Experimental source: clone E29.1
R/Tonnelie, C.
submitted to the EMBL Data Library, May 1990
A/Reference number: S70426
A/Accession: S70426

Query Match 37.4%; Score 539; DB 2; Length 109;
Best Local Similarity 93.6%; Pred. No. 1.3e-29;
Matches 102; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 152 SSELTDQPAVSVALGQTVRAITCGDSLRSYYASWYQKPGQAPVLVIYGNRRPSGIPDR 211
DB 1 SSELTDQPAVSVALGQTVRAITCGDSLRSYYASWYQKPGQAPVLVIYGNRRPSGIPDR 60
QY 212 FSGSSGNTASLTITGAQAEADYYCNSRDSGNHVFEGGQTKLTVLG 260
DB 61 FSGSYFGNTASLTITGAQAEADYYCNSRDSGNHVFEGGQTKLTVLG 109

RESULT 9
S25748
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25748
R;Combiarto, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25748
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-233 <COM>
A;Cross-references: UNIPARC:UPI0000115EFC; EMBL:X57813; NID:G33725; PIDN:CAA40950.1; PID
C;Superfamily: Immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;148-216/Domain: immunoglobulin homology <IMM>

Query Match 36.8%; Score 530.5; DB 2; Length 233;
Best Local Similarity 83.5%; Pred. No. 1.1e-28;
Matches 106; Conservative 6; Mismatches 10; Indels 5; Gaps 2;

QY 152 SSELTDQPAVSVALGQTVRAITCGDSLRSYYASWYQKPGQAPVLVIYGNRRPSGIPDR 211
DB 20 SSELTDQPAVSVALGQTVRAITCGDSLRSYYASWYQKPGQAPILVIYGNRRPSGIPDR 79
QY 212 FSGSSGNTASLTITGAQAEADYYCNSRDSGNHVFEGGQTKLTVLG---AAAEQKLI 268
DB 80 FSGSSGNTASFAITGAQAEADYYCNSRDSGQVLFEGGQTKLTVLGQPKAAPSVTLF 139
QY 269 --SEEDL 273
DB 140 PPSSEEL 146

RESULT 10
L3HUSH
Ig lambda chain V-III region (Sh) - human
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C;Accession: A01980
R;Titani, K.; Wikler, M.; Shinoda, T.; Putnam, F.W.
J. Biol. Chem. 245, 2171-2176, 1970
A;Title: The amino acid sequence of a lambda type Bence-Jones protein. III. The complete
A;Reference number: A92057; MUID:70166723; PMID:4909564
A;Accession: A01980
A;Molecule type: protein
A;Residues: 1-108 <TIT>
A;Cross-references: UNIPROT:P01714; UNIPARC:UPI000012E9FC
A;Note: the sequence of the C region is also given
C;Genetics:
A;Gene: GDB:IGLV@
A;Cross-references: GDB:119342; OMIM:147240
A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

F;14-88/Domain: immunoglobulin homology <IMM>
F;21-86/Diulfide bonds: #status experimental

Query Match 36.6%; Score 527; DB 1; Length 108;
Best Local Similarity 92.6%; Pred. No. 8.2e-29;
Matches 100; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 153 SELTQDPVAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIYGNRRPSGIPDRP 212
DB 1 SELTQDPVAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIYGNRRPSGIPDRP 60

QY 213 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLG 260
DB 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLG 108

RESULT 11

JC5322
P53 specific single-chain antibody Pab421 - human
C;Species: Homo sapiens (man)
C;Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997
C;Accession: JC5322
R;Jannot, C.B.; Hynes, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A;Title: Characterization of scFv-421, a single-chain antibody targeted to p53.
A;Reference number: JC5322; MUID: 97168950; PMID: 9016755
A;Molecule type: mRNA
A;Residues: 1-233 <JAN>
A;Cross-references: UNIPARC:UPI000017C2DE
A;Experimental source: hydricloma cell
C;Comment: This protein specifically binds the tumor suppressor protein p53. It restores

Query Match 36.3%; Score 522.5; DB 2; Length 233;
Best Local Similarity 49.0%; Pred. No. 3.6e-28;
Matches 117; Conservative 32; Mismatches 75; Indels 15; Gaps 8;

QY 28 ESGGQVVRPGSLRLSCAASGFTPDYGMVWVROAPKGLVSWGGINWGGSTGYADSVK 87
DB 2 ESGAELVRSGASVKSLCTTGFINDIYMHVWVKRPEQGLEWIGIPENDGADMTRSSG 61

QY 88 GRFTISRDNAKNSLYLQWNSLRARDTAVYVC-AMRAPVTVGQGTTLTVSRGGSGGGG 146
DB 62 VKATWTADTSNTAYLQLSLETSDTAVYCNAGMD---YWGQTTTVTSVSGGGSGGRA 118

QY 147 SGGGSS-ELTQDPA-VSVALGQTVRITCGD---SLRSY-YASWYQKPGQAPVLVIY 200
DB 119 SGGGSDIELTQSPASLAVSLGQRATISCRASKSVSTSGYSYMHWNQKPGQPPRLLIYL 178

QY 201 KNNRPSGIPDRFSGSSGNTASLTITGAQAEADYYC-NSRDSSGNHVVFGGTKLTV 258
DB 179 VSNLESGVPAFSGSGSGTDTFLNHPVBEADATYYCQHIRELTRSE---GGTKLEI 233

RESULT 12

S19672
Ig lambda chain V region (clone alpha-TSL14) - human
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C;Accession: S19672
R;Marks, J.D.; Hoogenboom, H.R.; Bonner, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph
A;Reference number: S19663; MUID: 92085276; PMID: 1748994
A;Accession: S19672
A;Molecule type: mRNA
A;Residues: 1-110 <MAR>
A;Cross-references: UNIPARC:UPI0000115FE3; EMBL:X61644; NID:g37856; PIDN:CAA43825.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-89/Domain: immunoglobulin homology <IMM>

Query Match 36.0%; Score 518.5; DB 2; Length 110;

Best Local Similarity 91.8%; Pred. No. 3.1e-28;
Matches 101; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 152 SSELTDQPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIYGNRRPSGIPDR 211
DB 1 SSELTDQPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIYGNRRPSGIPDR 60

QY 212 FSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLG 260
DB 61 FSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLG 110

RESULT 13

S02083
Ig lambda chain V-IV region - human (tentative sequence) (fragments)
N;Alternate names: amyloid-fibril protein GIL
C;Species: Homo sapiens (man)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 31-Mar-2000
C;Accession: S02083
R;Fykse, E.M.; Sletten, K.; Husby, G.; Cornwell III, G.G.
Biochem. J. 256, 973-980, 1988
A;Title: The primary structure of the variable region of an immunoglobulin IV light-chain
A;Reference number: S02083; MUID: 89134210; PMID: 3146981
A;Accession: S02083
A;Molecule type: protein
A;Residues: 1-70171-72173-75;76-131;132-146 <FYK>
A;Cross-references: UNIPARC:UPI0000176830; UNIPARC:UPI0000176831; UNIPARC:UPI0000176832;
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-88/Domain: immunoglobulin homology <IMM>

Query Match 36.0%; Score 518; DB 2; Length 146;
Best Local Similarity 82.7%; Pred. No. 4.5e-28;
Matches 105; Conservative 8; Mismatches 8; Indels 6; Gaps 3;

QY 153 SELTQDPVAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIYGNRRPSGIPDRP 212
DB 1 SELTQDPVAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIYGNRRPSGIPBRP 60

QY 213 SGSSSGNTASLTITGAQAEADYYCNSRDSSGN-HVFGGQTKLTVLG---AAAEQKLI 268
DB 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVIFGGQTKLTVLSQPKAAPSVTLF 120

QY 269 --SEEDL 273
DB 121 PPSSEEL 127

RESULT 14

S26928
Ig heavy chain V region (DP-32) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26928
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26985; MUID: 93021117; PMID: 1404388
A;Accession: S26928
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: UNIPARC:UPI0000116409; EMBL:Z12334; NID:g32887; PIDN:CAA78204.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 35.6%; Score 513; DB 2; Length 98;
Best Local Similarity 98.0%; Pred. No. 6.4e-28;
Matches 96; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 23 EVOLVESGGVVRPGSLRLSCAASGFTPDYGMVWVROAPKGLVSWGGINWGGSTGY 82
|||||

```
Db      1  EVQLVESGGGVVRRPGGSLRLSCAASGFTFDYGMHWVRQAPGKGLEWVSGINWNGSGTGY 60
Qy      83  ADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCAR 120
      |||
Db      61  ADSVKGRFTISRDNKNSLYLQMSLRAEDTALYYCAR 98
      |||

RESULT 15
S31595
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31595
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31595
A:Accession: S31595
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-128 <CUI>
A:Cross-references: UNIPARC:UPI0000116458; EMBL:Z14171; NID:g31007; PIDN:CAA78540.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;23-106/Domain: immunoglobulin homology <IMM>

Query Match      35.5%; Score 510.5; DB 2; Length 128;
Best Local Similarity 83.3%; Pred. No. 1.2e-27;
Matches 100; Conservative 6; Mismatches 7; Indels 7; Gaps 2;

Qy      23  EVQLVESGGGVVRRPGGSLRLSCAASGFTFDYGMHWVRQAPGKGLEWVSGINWNGSGTGY 82
      |||
Db      9   EVQLVESGGGVVRRPGGSLRLSCAASGFTFDYGMHWVRQAPGKGLEWVSGINWNGSGTGY 68
      |||

Qy      83  ADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARMAP-----VINGQGLVTVS 136
      |||
Db      69  ADSVKGRFTISRDNKNSLYLQMSLRAEDTALYYCAK-DAPGDHDAFDINGQGLVTVS 127
      |||
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Search completed: November 18, 2005, 21:47:22
Job time : 28.0883 secs

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Result No.	Score	Query Match	Length	DB	ID	Description	SUMMARIES	
1	758	52.6	240	2	Q65ZC9_HUMAN	Q65zc9 homo sapien		
2	715	49.7	255	2	Q6XB05_MOUSE	Q6xb05 mus musculus		
3	695.5	48.3	248	2	Q65ZQ7_9MUR1	Q65zq7 mus sp. b3 (
4	636	44.2	244	2	Q65ZC8_HUMAN	Q65zc8 homo sapien		
5	600	41.7	245	2	Q921A6_MOUSE	Q921a6 mus musculus		
6	578	40.1	243	2	Q7TQM2_MOUSE	Q7tqm2 mus musculus		
7	552	38.3	107	2	Q9NSD6_HUMAN	Q9nsd6 homo sapien		
8	550.5	38.2	112	2	Q9HCC1_HUMAN	Q9hcc1 homo sapien		
9	548	38.1	487	2	Q65ZL2_9MUR1	Q65z12 mus sp. fv/		
10	530	36.8	233	2	Q6GMW4_HUMAN	Q6gmw4 homo sapien		
11	527	36.6	108	1	LV3A_HUMAN	P01714 homo sapien		
12	516	35.8	472	2	Q6N089_HUMAN	Q6n089 homo sapien		
13	511	35.5	499	2	Q8NSK4_HUMAN	Q8nsk4 homo sapien		
14	509.5	35.4	469	2	Q569F4_HUMAN	Q569f4 homo sapien		
15	508	35.3	573	2	Q8WU38_HUMAN	Q8wu38 homo sapien		
16	507.5	35.2	218	2	Q925S1_MOUSE	Q925s1 mus musculus		
17	504	35.0	97	2	Q5NV73_HUMAN	Q5nv73 homo sapien		
18	483	33.5	121	2	Q9UL71_HUMAN	Q9ul71 homo sapien		
19	478	33.2	470	2	Q6FUA4_HUMAN	Q6fua4 homo sapien		
20	478	33.2	478	2	Q6P181_HUMAN	Q6p181 homo sapien		
21	477	33.1	606	2	Q6GMY2_HUMAN	Q6gmy2 homo sapien		
22	474	32.9	464	2	Q6WZU6_HUMAN	Q6wzu6 homo sapien		
23	474	32.9	613	2	Q8WUK1_HUMAN	Q8wuk1 homo sapien		
24	473.5	32.9	597	2	Q96BB9_HUMAN	Q96bb9 homo sapien		
25	471.5	32.7	473	2	Q6WZV7_HUMAN	Q6wzv7 homo sapien		
26	470	32.6	113	2	Q9UL90_HUMAN	Q9ul90 homo sapien		
27	465	32.3	493	2	Q6GMX2_HUMAN	Q6gmx2 homo sapien		
28	461.5	32.0	118	2	Q9UL91_HUMAN	Q9ul91 homo sapien		
29	457.5	31.8	475	2	Q6MZQ6_HUMAN	Q6mzq6 homo sapien		
30	456	31.7	466	2	Q61N78_HUMAN	Q61n78 homo sapien		
31	452.5	31.4	479	2	Q6MZV6_HUMAN	Q6mzv6 homo sapien		

Best Local Similarity 50.8%; Pred. No. 3.6e-38;
Matches 124; Conservative 46; Mismatches 64; Indels 10; Gaps 4;

Qy 23 EVOLVSGGGVVRPGGSLRLSCAASGFTFDDYGMWVRQAPGKGLVWVGGINWNGSGTG 82
Db 1 QVOLVSGAEVKKPGDGVKVCASGYTSDHYHWMVRQAPGKGLVWVGWIDPNNGDTRF 60

Qy 83 ADSVKGRFTISRDNKNSLYLQWNSLRAEDTAVYYCAR-----MRAPVINGQGLTVTVS 136
Db 61 AQRFGQRTVMTSDTSIAAYMEVSLRSDTAVYYCAREGTGSAIYGMVDMVQGLTVTVS 120

Qy 137 RGGGGGGGGGGSS-ELTQDPA-VSVALGQTVRITCGDLSRSYASWYQKPGQAP 194
Db 121 SGGGGGGGGGGGSDIQMTQSPSTLSASIGDRVTITCRASEGYHHLAWYQKPGKAP 180

Qy 195 VLVIYKNNRPSGIPDRFSGSSGNTASLTITGAQAEADYVNCNSRDSSGNHVVFGGT 254
Db 181 KFLIYKASSLASAPRFGSGSGTDTLTISLQDDPATYIC--QQVSNYPLTFGGGT 238

Qy 255 KLTV 258
Db 239 KLEI 242

RESULT 5
Q921A6 MOUSE
ID Q921A6 MOUSE PRELIMINARY; PRT; 241 AA.
AC Q921A6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-CEA 79 single chain Fv (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98170165; PubMed=9509426;
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D., Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and generation of a single-chain Fv molecule (scFv).";
RM Mol. Cells 7:816-819(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91341421; PubMed=1908510; DOI=10.1084/jem.174.3.613;
RA Stark S.E., Caton A.J.;
RT "Antibodies that are specific for a single amino acid interchange in a protein epitope use structurally distinct variable regions.";
RJ J. Exp. Med. 174:613-624(1991).
DR EMBL; U88067; AAB48044.1; -; mRNA.
DR PIR; S19965; S19965.
DR PIR; S19967; S19967.
DR PIR; S19968; S19968.
DR PIR; S26325; S26325.
DR HSP; P01607; IBW.
DR Ensembl; ENSMUSG0000021155; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IG; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 1 241
FT SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

Query Match 41.7%; Score 600; DB 2; Length 241;
Best Local Similarity 51.9%; Pred. No. 1.4e-35;
Matches 126; Conservative 34; Mismatches 67; Indels 16; Gaps 6;

Qy 23 EVOLVSGGGVVRPGGSLRLSCAASGFTFDDYGMWVRQAPGKGLVWVGGINWNGSGTG 82

Db 137 SGGGGGGGGRIQWTOFASLSVSGELVITTCRASENIYSNLAWYQKQKSPQLIVY 196
Qy 200 GKNNRPSGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGKTLTV 258
Db 197 AATNLADGVPRFSGSGSTQYSLKNSQSEDYFSGYYC--QHWGTPTPTFGGGRLEI 253

RESULT 10

Q6GMW4 HUMAN
ID Q6GMW4 HUMAN PRELIMINARY; PRT; 233 AA.
AC Q6GMW4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]

NUCLEOTIDE SEQUENCE

RP TISSUE=Primary B-Cells;
RX MEDLINE=2238625; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiech F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]

NUCLEOTIDE SEQUENCE

RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073786; AAH73786.1; -, mRNA.
DR SMR; Q6GMW4; 23-229.
DR GO; GO:0005489; P:electron transport activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.

INTERPRO

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003597; IG cl.

DR InterPro; IPR003006; IG_MHC.

DR InterPro; IPR003596; IG_v.

DR Pfam; PF07654; Cl-set; 1.

DR SMART; SM00409; IG; 2.

DR SMART; SM00406; IGV; 1.

DR SMART; SM00407; IGcl; 1.

DR PROSITE; PS00835; IG LIKE; 2.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

KW Hypothetical protein.

SQ SEQUENCE 233 AA; 24855 MW; 462677B3B8FDE5D CRC64;

Query Match

Best Local Similarity 36.8%; Score 530; DB 2; Length 233;

Matches 100; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 152 SSELTPAVSVVALGQTVRTTCQDLSRYSYASWYQKPGQAPVLVIYGNRPSGIPDR 211

Db 20 SSELTPAVSVVALGQTVRTTCQDLSRYSYASWYQKPGQAPVLVIYGNRPSGIPDR 79
Qy 212 FSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGKTLTVLG 260
Db 80 FSGSGSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGKTLTVLG 128

RESULT 11

LV3A HUMAN
ID LV3A HUMAN STANDARD; PRT; 108 AA.
AC P01714;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig lambda chain V-III region SH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]

PROTEIN SEQUENCE

RX MEDLINE=70166723; PubMed=4909564;
RA Titani K., Wikler M., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a lambda type Bence-Jones protein. 3. The
RT complete amino acid sequence and the location of the disulfide
RT bridges."
RL J. Biol. Chem. 245:2171-2176(1970).
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

DR PIR; A01980; L3HUSH.

DR HSP; P01703; 7PAB.

DR GO; GO:0005576; C:extracellular region; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003596; IG_v.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG LIKE; 1.

KW Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;

KW Immunoglobulin V region.

FT DOMAIN 1 97 IG-like.

FT DISULFID 21 86

FT NON TER 108 108

SQ SEQUENCE 108 AA; 11393 MW; E7E1229586411A56 CRC64;

Query Match

Best Local Similarity 36.6%; Score 527; DB 1; Length 108;

Matches 100; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 153 SELTPAVSVVALGQTVRTTCQDLSRYSYASWYQKPGQAPVLVIYGNRPSGIPDRF 212

Db 1 SELTPAVSVVALGQTVRTTCQDLSRYSYASWYQKPGQAPVLVIYGNRPSGIPDRF 60

Qy 213 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGKTLTVLG 260

Db 61 SGSSSGHTASLTITGAQAEADYYCNSRDSSGNHVVFGGKTLTVLG 108

RESULT 12

Q6N089 HUMAN
ID Q6N089 HUMAN PRELIMINARY; PRT; 472 AA.
AC Q6N089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

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DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypochemical protein DKFp686f15220.
GN Name=DKFp686f15220;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Rectum tumor;
RG The German cDNA Consortium;
RA Wambutt R., Heubner D., Newes H.W., Weil B., Amid C., Oeanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640627; CAB45781.1; -; mRNA.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypochemical protein.
SQ
SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 35.8%; Score 516; DB 2; Length 472;
Best Local Similarity 47.3%; Pred. No. 3.7e-29;
Matches 116; Conservative 20; Mismatches 77; Indels 32; Gaps 5;

QY 13 LLLAQAQPAAMAEVQLVESGGGVVPGGSLRLSCAASGFTEDDYGMVWVRQAPGKLEWVSG 72
DB 10 LLAILGVQCEVLVESGGGVVPGGSLRLSCAASGFTEDDYGMVWVRQAPGKLEWVSG 69

QY 73 INWGGSTGYADSVKGRFTISRDNKNSLYLQWNSLRAEDTAVYYCAR-----MRAP 124
DB 70 ISWNSGSIAYADSVKGRFTISRDNKNSLYLQWNSLRAEDTALYYCAKEIGHNFFYYGM 129

QY 125 VINGQGLTVTSRGGGSGGGGGGGSSSELTPDPAVSVVALQGVITCGDLSRYYAS 184
DB 130 DVWGQGLTTVTS-----SASTKGPSVFPLAPSSKSTSGGTAALGCL-LVKDYFPE 177

QY 185 WYQKPKQAPVLYVIGNKRRPSGI---PDRFSGSSSGNTASLITGAQAEDEADYYCNSR 241
DB 178 -----PVTVSNWNGALTSVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVN 228

QY 242 DSSGN 246
DB 229 HKPSN 233

RESULT 13
ID Q8N5K4 HUMAN PRELIMINARY; PRT; 499 AA.
AC Q8N5K4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MGC27165 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Blood;
RG MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

```

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauser R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleks U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Blood;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032249; AAH32249.1; -; mRNA.
DR HSSP; P01876; 1OW0.
DR SMR; Q8N5K4; 269-477.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 2.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Immunoglobulin domain; Repeat.
SQ
SEQUENCE 499 AA; 53376 MW; 93A5C89582054F32 CRC64;

Query Match 35.5%; Score 511; DB 2; Length 499;
Best Local Similarity 49.6%; Pred. No. 9.1e-29;
Matches 121; Conservative 16; Mismatches 49; Indels 58; Gaps 8;

QY 13 LLLAQAQPAAMAEVQLVESGGGVVPGGSLRLSCAASGFTEDDYGMVWVRQAPGKLEWVSG 72
DB 10 LLAILGVQCEVLVESGGGVVPGGSLRLSCATSGFTEDDSGASWVRQAPGKLEWVSS 69

QY 73 INWGGSTGYADSVKGRFTISRDNKNSLYLQWNSLRAEDTAVYYCARWAPV----- 125
DB 70 INWGGSTGYADSVKGRFTISRDNKNSLYLQWNSLRAEDTALYYCARDPTKYCSGGSCL 129

QY 126 -----IWGQGLTVTSRGGGSGGGGGSSSELTPDPAVSVVALQGVITCGDLSRYYAS 173
DB 130 GYMDVWGKTTVTS-----SASPTSPKVPFLSLCSTQPDGNVVLACL 174

QY 174 QGDSLSYYASWYQQKP-----GQAPVLYVIGNKRRPSGIPDRFSGSSSGNTASLTI 225
DB 175 QG-----FPQEPFLSVTSSESQGG---VTARNFFPS---QDASGDLYTTSQTL 218

QY 226 TGAQ 229
DB 219 PATQ 222

RESULT 14
ID Q569F4 HUMAN PRELIMINARY; PRT; 469 AA.
AC Q569F4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE IGHG1 protein.

```


QY	174	QGDLSRYSYASWYQKPGQAPVLVIYKNNRPS-GIPDRFSGSSGNTASLTITGAQAE	232
Db	174	TGYHTSVTVIWM-----GTQSQPORTPFIQRRDSYINTSSQLSTPLQQR	221
QY	233	EADYYC	238
Db	222	QGEYKC	227

Search completed: November 18, 2005, 21:53:33
Job time : 160.161 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2005, 21:17:08 ; Search time 61.6278 Seconds
(without alignments)
791.381 Million cell updates/sec

Title: US-10-029-926d-7

Perfect score: 576

Sequence: 1 SELTQDPAPVAVLQQTVRIT.....SGNHWFGGKTKLTVLGAAA 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_21:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*
- 9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	576	100.0	111	5	ABG78132 Human Fv
2	576	100.0	111	5	ABG91823 Human ant
3	576	100.0	112	8	ADJ57867 Common li
4	576	100.0	125	9	ADW88761 Hepatitis
5	576	100.0	209	5	AAU98017 Human ace
6	576	100.0	244	9	ADW90315 Phage scf
7	576	100.0	244	9	ADW90315 SARS coro
8	576	100.0	247	9	ADW90312 Phage scf
9	576	100.0	247	9	ADW90312 SARS coro
10	576	100.0	249	8	ADR23324 Human CD7
11	576	100.0	260	5	ABG92023 Antibody
12	576	100.0	263	5	ABG92024 Antibody
13	576	100.0	266	5	ABG92020 Human ant
14	576	100.0	277	5	ABG78150 Human Fv
15	576	100.0	277	5	ABG78328 Human Fv
16	576	100.0	277	5	ABG92019 Human ant
17	576	100.0	277	5	ABG91841 Human ant
18	576	100.0	277	8	ADI28366 Human scf
19	576	100.0	277	8	ADW82026 Human pla
20	576	100.0	278	8	ADI28367 Human scf
21	576	100.0	278	8	ADS82027 Human pla
22	576	100.0	280	4	AAE02186 PAM2 sing
23	576	100.0	280	8	ADI28368 Human scf
24	576	100.0	280	8	ADJ57363 P-selectin

25	576	100.0	280	8	ADS82028 Human leu
26	576	100.0	280	8	ADT63078 Human scf
27	576	100.0	280	9	ADX01180 Amino aci
28	576	100.0	280	9	ADX01181 Amino aci
29	576	100.0	280	9	ADX01131 Amino aci
30	576	100.0	280	9	ADX01130 Amino aci
31	576	100.0	280	9	ADX01185 Amino aci
32	576	100.0	280	9	ADX01186 Amino aci
33	576	100.0	280	9	ADY78380 Amino aci
34	576	100.0	280	9	ADY78325 Single ch
35	576	100.0	280	9	ADY78324 Single ch
36	576	100.0	280	9	ADY78379 Single ch
37	576	100.0	280	9	ADY78374 Single ch
38	576	100.0	280	9	ADY78375 Single ch
39	576	100.0	282	4	AAE02185 PAM1 sing
40	576	100.0	309	2	AAW83322 Single ch
41	576	100.0	309	5	ABB09603 Amino aci
42	576	100.0	309	6	ABG74384 Single ch
43	576	100.0	309	7	ADG98737 Human sin
44	576	100.0	309	8	ADO40446 Human sin
45	576	100.0	312	2	AAW83323 Single ch

ALIGNMENTS

RESULT 1

ABG78132
ID ABG78132 standard; protein; 111 AA.

AC ABG78132;

DT 15-NOV-2002 (first entry)

XX Human Fv molecule hypervariable region related peptide #7.

DE Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
XX Homo sapiens.
OS WO200259264-A2.
PN 01-AUG-2002.
PD 31-DEC-2001; 2001WO-US049440.
PF 29-DEC-2000; 2000US-00751181.
PR (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
XX Plaksin D, Peretz T;
XX WPI; 2002-619166/66.
XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
FT or fragment, or construct of fragment with enhanced binding
FT characteristics so as to selectively bind target cell in favor of other
FT cells.
XX Disclosure; Page 150; 232pp; English.
XX The invention relates to a peptide or polypeptide comprising an Fv
CC molecule, a construct or fragments or a construct of a fragment with
CC enhanced binding characteristics which selectively and/or specifically
CC binds to a target cell in favour of other cells, where binding is
CC primarily determined by a first hypervariable region and Fv is a single
CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
CC association with or attached, coupled, combined, linked or fused to a
CC pharmaceutical agent, is useful in the manufacture of a medicament, where
CC the medicament has activity against a diseased cell, preferably a cancer

CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
 CC composition for use in inhibiting the growth of a diseased or cancer
 CC cell. This sequence represents a human Fv molecule hypervariable region
 CC related peptide of the invention
 XX
 SQ Sequence 111 AA;

Query Match 100.0%; Score 576; DB 5; Length 111;
 Best Local Similarity 100.0%; Pred. No. 3.2e-35;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTQDPVAVSVALGQTVRITCQDLSRSYASWYQKPGQAPVLVIYGNRPSGIPDRF 60
 DB 1 SELTQDPVAVSVALGQTVRITCQDLSRSYASWYQKPGQAPVLVIYGNRPSGIPDRF 60
 QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGAAA 111
 DB 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGAAA 111

RESULT 2
 ABG91823
 ID ABG91823 standard; protein; 111 AA.

XX ABG91823;

DT 04-DEC-2002 (first entry)

XX Human antibody fragment #7.

XX Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
 KW metastasis; hypervariable region; autoimmune disease; thrombosis;
 KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
 KW myocardial infarction; retinopathic disease; abnormal platelet function;
 KW sulphated tyrosine-dependent protein-protein interaction.

XX Homo sapiens.

XX WO200253700-A2.

XX 11-JUL-2002.

XX 31-DEC-2001; 2001WO-US049442.

XX 29-DEC-2000; 2000US-00751181.

XX 29-DEC-2000; 2000US-0258948P.

XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX Lazarovits J, Hagai Y, Plakain D, Vogel T, Nimrod A, Mar-Haim H;
 XX Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
 XX WPI; 2002-674776/72.

XX Novel isolated epitope present on cancer cells and important in
 XX physiological phenomena such as cell rolling, metastasis and
 XX inflammation, for treating autoimmune, inflammatory or cardiovascular
 XX diseases, and cancer.

XX Disclosure; Page 227-228; Opp; English.

XX The invention relates to an isolated epitope present on cancer cells and
 XX important in physiological phenomena such as cell rolling, metastasis and
 XX inflammation, where the epitope is capable of being bound by an antibody,
 XX its antigen-binding fragment or its complex comprising at least one
 XX antibody or its binding fragment having a first hypervariable region. The
 XX epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 XX disease, thrombosis, restenosis, metastasis, growth and/or replication of
 XX tumour or leukaemia cells, increase in number of tumour or leukaemia
 XX cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 XX platelet and/or cell-platelet adhesion or aggregation, for increasing

CC mortality of tumour or leukaemia cells, for increasing the susceptibility
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia
 CC cells in a patient, or in the manufacture of a medicament for the above
 CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents a human antibody fragment
 CC of the invention
 XX
 SQ Sequence 111 AA;

Query Match 100.0%; Score 576; DB 5; Length 111;
 Best Local Similarity 100.0%; Pred. No. 3.2e-35;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTQDPVAVSVALGQTVRITCQDLSRSYASWYQKPGQAPVLVIYGNRPSGIPDRF 60
 DB 1 SELTQDPVAVSVALGQTVRITCQDLSRSYASWYQKPGQAPVLVIYGNRPSGIPDRF 60
 QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGAAA 111
 DB 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGAAA 111

RESULT 3
 ADJ57867

ID ADJ57867 standard; protein; 112 AA.

XX ADJ57867;

XX 06-MAY-2004 (first entry)

XX Common light variable chain protein of B28, II-2 and I-2.

XX Cytostatic; Immunosuppressive; Antibacterial; Virucide; Fungicide;
 KW Antiparasitic; auto-immune disease; cancer; neoplastic disorder;
 KW leukaemia.

XX Synthetic.

XX WO2004009618-A2.

XX 29-JAN-2004.

XX 15-JUL-2003; 2003WO-EP007690.

XX 18-JUL-2002; 2002EP-00077953.

XX 18-JUL-2002; 2002US-0397066P.

XX 27-MAY-2003; 2003WO-EP050201.

XX (CRUC-) CRUCELL HOLLAND BV.

XX Van Berkel PHC, Brus RHP, Bout A, Logtenberg T;
 XX WPI; 2004-132914/13.

XX N-PSDB; ADJ57866.

XX Producing mixture of antibodies in recombinant host comprises expressing
 XX nucleic acid sequence(s) encoding light chain and three different heavy
 XX chains capable of pairing with light chain in recombinant host cell.

XX Disclosure; SEQ ID NO 18; 186pp; English.

XX The present invention relates to producing a mixture of antibodies in a
 XX recombinant host comprises expressing in a recombinant host cell a
 XX nucleic acid sequence or nucleic acid sequences encoding a light chain
 XX and at least three different heavy chains that are capable of pairing
 XX with a light chain. The method is useful for producing a mixture of
 XX antibodies in a recombinant host, is useful for the preparation of a
 XX medicament for use in the treatment or diagnosis of a disease or disorder

CC in a human or animal. The antibodies are useful for treating auto-immune
 CC disease and cancer such as solid tumors of the brain, head and neck,
 CC breast, prostate, colon, lung, etc., hematologic tumors such as B-cell
 CC tumors, neoplastic disorders such as leukemia, lymphoma, sarcoma,
 CC carcinoma, neural cell tumors, myelomas, melanomas, neuroblastomas, etc,
 CC and are also useful for treating graft-versus-host rejections, infectious
 CC diseases due to pathogenic bacteria such as multidrug resistant
 CC Staphylococcus aureus, fungi such as Candida albicans, as prophylaxis
 CC against viruses such as rabies virus, for treating or preventing disease
 CC caused by adenoviruses, respiratory syncytium virus, and for treating
 CC diseases caused by unicellular or multicellular parasites. The method
 CC enables exploring many combinations simultaneously, where the
 CC combinations include the presence of bispecific antibodies in the
 CC produced mixture. The present sequence represents the common light
 CC variable chain of B28, II-2 and I-2.
 XX
 SQ Sequence 112 AA;

Query Match 100.0%; Score 576; DB 8; Length 112;
 Best Local Similarity 100.0%; Pred. No. 3.2e-35;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SELTQDPAVSVALGQTVRITTCQGSLSRSYASWYQKPGQAPVLVIYKNNRPSGIDPRF 60
 DB 2 SELTQDPAVSVALGQTVRITTCQGSLSRSYASWYQKPGQAPVLVIYKNNRPSGIDPRF 61
 QY 61 SGSSSGNTASLTITGAQAEADYCNRSRDSGNHVVFGGTKLTVLGAAA 111
 DB 62 SGSSSGNTASLTITGAQAEADYCNRSRDSGNHVVFGGTKLTVLGAAA 112

RESULT 4
 ADW88761
 ID ADW88761 standard; protein; 125 AA.
 XX
 AC ADW88761;
 XX
 XX 07-APR-2005 (first entry)
 XX Hepatitis B virus surface antigen scFv antibody.
 XX
 KW Analyte detection; microarray; hepatitis B virus surface antigen;
 KW single chain antibody; heavy chain variable region.
 XX
 OS Unidentified.
 XX
 XX W02005007893-A2.
 XX
 XX 27-JAN-2005.
 XX
 XX 09-JUL-2004; 2004WO-US021765.
 XX
 XX 10-JUL-2003; 2003US-0487018P.
 PR 06-OCT-2003; 2003US-0509196P.
 XX
 XX (BLIN-) BLIND PIG PROTEOMICS LLC.
 XX
 XX Cull MG, Brennan M, Gill R;
 PI
 XX WPI; 2005-152093/16.
 DR N-PSDB; ADW88759, ADW88760.
 XX
 XX Detecting binding, useful for detecting antigen:antibody complexes, by
 PT providing Physically Alterable Binding Reagent and ligand, and detecting
 PT conformational change in Physically Alterable Binding Reagent to detect
 PT binding to the ligand.
 XX
 PS Example 7; SEQ ID NO 8; 37pp; English.
 XX
 CC The invention relates to a universal detection system for ligand binding
 CC using a physically alterable binding reagent (PABR) and in some
 CC embodiments a universal detection reagent (UDR). A claimed method for
 CC detection of binding comprises: providing a PABR; providing a ligand,

CC where the PABR specifically binds to the ligand; and detecting a
 CC conformational change in the PABR, whereby binding of the PABR to the
 CC ligand is detected. The conformational change may be detected by:
 CC providing a UDR; and detecting binding of the UDR to the PABR. The
 CC detection may be quantitative. The PABR may comprise: a ligand binding
 CC site; a domain that becomes physically altered upon binding of ligand to
 CC the ligand binding site; and, optionally, a site useful for coupling the
 CC binding reagent to a solid support. The PABR may comprise an antibody or
 CC a receptor binding domain or a tag for coupling the PABR to a solid
 CC support. The antibody may be a monomeric IgM, oligomeric IgW, an Fab
 CC fragment, an F(ab)2 fragment, a genetically engineered antibody or a
 CC chimeric antibody. A further method for detecting binding comprises:
 CC preparing a microarray comprising a plurality of PABRs at specific
 CC locations on the surface of a solid support in an addressable format;
 CC providing a sample suspected of containing a ligand such that the PABR
 CC specifically binds to the ligand; providing a UDR; and detecting the
 CC binding of the UDR to the PABR. The methods are useful for detecting
 CC ligand binding, e.g. as diagnostics, research uses, and industrial
 CC applications. The methods are also useful in detecting antigen:antibody
 CC complexes on either protein or antibody microarrays. The present sequence
 CC is that of the light chain variable region of a hepatitis B virus surface
 CC antigen (HBsAg) single chain Fv antibody. An AvidTagged IgM antibody
 CC suitable for use as a PABR could be constructed using the variable heavy
 CC chain domain sequence and a light chain domain sequence (variable and
 CC constant regions) that together contain the HBsAg antibody domains.

XX SQ Sequence 125 AA;

Query Match 100.0%; Score 576; DB 9; Length 125;
 Best Local Similarity 100.0%; Pred. No. 3.6e-35;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTQDPAVSVALGQTVRITTCQGSLSRSYASWYQKPGQAPVLVIYKNNRPSGIDPRF 60
 DB 1 SELTQDPAVSVALGQTVRITTCQGSLSRSYASWYQKPGQAPVLVIYKNNRPSGIDPRF 60
 QY 61 SGSSSGNTASLTITGAQAEADYCNRSRDSGNHVVFGGTKLTVLGAAA 111
 DB 61 SGSSSGNTASLTITGAQAEADYCNRSRDSGNHVVFGGTKLTVLGAAA 111

RESULT 5
 AAU98017
 ID AAU98017 standard; protein; 209 AA.
 XX
 AC AAU98017;
 XX
 XX 27-AUG-2002 (first entry)
 XX Human acetylcholinesterase antibody PD-antiHASP 1.
 XX
 KW Human; synaptic acetylcholinesterase; PD-antiHASP 1; antibody;
 KW single-chain variable fragment; scFv; AChE-S;
 KW heavy chain variable region; progressive neuromuscular disorder;
 KW muscle distortion; muscle re-innervation; myasthenia gravis;
 KW neuromuscular junction abnormality; Eaton-Lambert disease;
 KW muscular dystrophy; amyotrophic lateral sclerosis; ALS;
 KW post-traumatic stress disorder; PTSD; multiple sclerosis; Dystonia;
 KW post-stroke sclerosis; post-injury muscle damage;
 KW excessive re-innervation.
 XX
 OS Homo sapiens.
 XX
 PN W0200246422-A1.
 XX
 XX 13-JUN-2002.
 XX
 XX 22-MAY-2001; 2001WO-IL000464.
 XX
 XX 04-DEC-2000; 2000IU-00140071.
 XX
 XX (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
 XX

PI Soreq H, Flores CF, Nissim A;
 XX WPI; 2002-463832/49.
 DR N-PSDB; ABK52915.
 XX
 XX Nucleic acid sequence coding for a single-chain variable fragment (scFv)
 PT antibody that has specific affinity for the synaptic variant of
 PT acetylcholinesterase (ACHE-S), useful for diagnosing a neuromuscular
 PT disorder, e.g. Myasthenia gravis.
 XX
 XX Claim 11; Page 61-63; 73pp; English.
 PS
 XX The invention relates to a nucleic acid sequence coding for a single-
 CC chain variable fragment (scFv) antibody that has specific affinity for
 CC the synaptic variant of acetylcholinesterase (ACHE-S), where the scFv
 CC antibody consists essentially of a polypeptide comprising the binding
 CC portion of the heavy chain variable region of an antibody. Also included
 CC are an expression vehicle comprising a nucleic acid sequence coding for a
 CC scFv antibody that has specific affinity for the synaptic variant of ACHE
 CC -S, an scFv antibody specifically recognising and binding to the synaptic
 CC variant of ACHE-S and a method for the diagnosis of a progressive
 CC neuromuscular disorder in a mammal, comprising obtaining a sample from
 CC the mammal and detecting intensified expression of at least one of the
 CC ACHE variants in the sample. The single-chain Fv antibody is useful for
 CC diagnosing a progressive neuromuscular disorder which involves any one of
 CC muscle distortion, muscle re-innervation and neuromuscular junction (NMJ)
 CC abnormalities. The disorder is Myasthenia gravis (preferred), Eaton-
 CC Lambert disease, muscular dystrophy, amyotrophic lateral sclerosis (ALS),
 CC post-traumatic stress disorder (PTSD), multiple sclerosis, Dystonia, post
 CC stroke sclerosis, post-injury muscle damage, excessive re-innervation,
 CC or post-exposure to ACHE inhibitors. The present sequence represents an
 CC anti-ACHE scFv antibody, PD-antiHASP 1
 XX
 SQ Sequence 209 AA;
 Query Match 100.0%; Score 576; DB 5; Length 209;
 Best Local Similarity 100.0%; Pred. No. 6e-35;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SELTQDPAVSVALGQTVRIITCQGSLSRSYASWYQKPGQAPVLVIYGNKRRPSGIPDRF 60
 Db 76 SELTQDPAVSVALGQTVRIITCQGSLSRSYASWYQKPGQAPVLVIYGNKRRPSGIPDRF 135
 QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGAAA 111
 Db 136 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGAAA 186
 RESULT 6
 ADW90315
 ID ADW90315 standard; protein; 244 AA.
 XX
 AC ADW90315;
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE Phage scFv SARS antibody SEQ ID NO 585.
 XX
 XX Virucide; Vaccine; diagnosis; Severe acute respiratory syndrome;
 KW respiratory-gen.; infection; respiratory disease; antibody.
 KW SARS coronavirus.
 OS
 PN WO2005012337-A2.
 XX
 XX 10-FEB-2005.
 XX
 XX 15-JUL-2004; 2004WO-EP051498.
 XX
 PR 15-JUL-2003; 2003WO-EP050308.
 PR 24-JUL-2003; 2003WO-EP050333.
 PR 02-SEP-2003; 2003WO-EP050392.
 PR 27-OCT-2003; 2003WO-EP050761.

PR 24-NOV-2003; 2003WO-EP050883.
 XX
 PA (CRUC-) CRUCELL HOLLAND BV.
 XX
 PI Ter Meulen JH, Goudsmit J, Slootstra JW, Timmerman P, De Kruif CA;
 PI Van Den Brink EN;
 XX WPI; 2005-162947/17.
 XX
 XX New antigenic peptides from severe acute respiratory syndrome-coronavirus
 PT (SARS-CoV), useful in preparing a composition for diagnosing, treating or
 PT preventing SARS-CoV infection.
 XX
 PS Example 2; SEQ ID NO 585; 199pp; English.
 XX
 XX The invention relates to an antigenic peptide from severe acute
 CC respiratory syndrome-coronavirus (SARS-CoV). The peptide or nucleic acid
 CC molecule encoding the peptide, fusion protein, conjugate or antibody is
 CC useful in preparing a composition for diagnosing, treating or preventing
 CC SARS-CoV infection. The present sequence represents a phage scFv SARS
 CC antibody.
 XX
 SQ Sequence 244 AA;
 Query Match 100.0%; Score 576; DB 9; Length 244;
 Best Local Similarity 100.0%; Pred. No. 7e-35;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SELTQDPAVSVALGQTVRIITCQGSLSRSYASWYQKPGQAPVLVIYGNKRRPSGIPDRF 60
 Db 134 SELTQDPAVSVALGQTVRIITCQGSLSRSYASWYQKPGQAPVLVIYGNKRRPSGIPDRF 193
 QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGAAA 111
 Db 194 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGAAA 244
 RESULT 7
 ADX01815
 ID ADX01815 standard; protein; 244 AA.
 XX
 AC ADX01815;
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE SARS coronavirus scFv antibody SEQ ID NO 71.
 XX
 KW severe acute respiratory syndrome; diagnosis; Respiratory-Gen.; Virucide;
 KW respiratory disease; infection; antibody.
 XX
 OS SARS coronavirus.
 XX
 PN WO2005012360-A2.
 XX
 XX 10-FEB-2005.
 XX
 XX 21-JUL-2004; 2004WO-EP051568.
 XX
 PR 22-JUL-2003; 2003WO-EP050328.
 PR 01-SEP-2003; 2003WO-EP050391.
 PR 16-OCT-2003; 2003WO-EP050723.
 PR 24-NOV-2003; 2003WO-EP050883.
 PR 04-DEC-2003; 2003WO-EP050943.
 PR 02-FEB-2004; 2004WO-EP050067.
 PR 13-FEB-2004; 2004WO-EP050127.
 PR 19-MAR-2004; 2004WO-EP050334.
 PR 07-APR-2004; 2004WO-EP050464.
 PR 14-APR-2004; 2004WO-EP050516.
 PR 29-APR-2004; 2004WO-EP050643.
 XX
 XX (CRUC-) CRUCELL HOLLAND BV.
 XX
 XX Ter Meulen JH, De Kruif CA, Van Den Brink EN, Goudsmit J;

XX WPI; 2005-142879/15.
 DR N-PSDB; ADX01814.
 XX
 PT New binding molecules that specifically bind to severe acute respiratory
 PT syndrome (SARS)-coronavirus (CoV), useful for diagnosing, preventing or
 PT treating conditions resulting from SARS-CoV.
 XX
 XX Example 3; SEQ ID NO 71; 633pp; English.
 XX
 XX The invention relates to a binding molecule, or its variant, capable of
 CC specifically binding to a severe acute respiratory syndrome (SARS)-
 CC coronavirus (CoV). The composition (including the binding molecule or its
 CC functional variant, or the immunoconjugate) is useful as a medicament for
 CC the diagnosis, prophylaxis or treatment of a condition resulting from a
 CC SARS-CoV, or in the preparation of the medicament. The present sequence
 CC represents a SARS coronavirus scFv.
 XX
 XX Sequence 244 AA;
 SQ
 Query Match 100.0%; Score 576; DB 9; Length 244;
 Best Local Similarity 100.0%; Pred. No. 7e-35;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 Qy 1 SELTQDPAVSVALGQTVRITTCQGSLSRSYASWTQKPGQAPVLVIYKNNRPSGIDPRF 60
 Db |||||
 Qy 61 SGSSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGKTLTVLGAAA 111
 Db |||||
 Qy 194 SGSSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGKTLTVLGAAA 244
 Db |||||
 RESULT 8
 ID ADW90312 standard; protein; 247 AA.
 XX
 AC ADW90312;
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE Phage scFv SARS antibody SEQ ID NO 582.
 XX
 KW Virucide; Vaccine; diagnosis; Severe acute respiratory syndrome;
 KW respiratory-gen.; infection; respiratory disease; antibody.
 XX
 OS SARS coronavirus.
 XX
 PN WO2005012337-A2.
 XX
 PD 10-FEB-2005.
 XX
 PF 15-JUL-2004; 2004WO-EP051498.
 XX
 PR 15-JUL-2003; 2003WO-EP050308.
 PR 24-JUL-2003; 2003WO-EP050333.
 PR 02-SEP-2003; 2003WO-EP050392.
 PR 27-OCT-2003; 2003WO-EP050761.
 PR 24-NOV-2003; 2003WO-EP050883.
 XX
 XX (CRUC-) CRUCCELL HOLLAND BV.
 XX
 XX Ter Meulen JH, Goudsmit J, Slootstra JW, Timmerman P, De Kruif CA;
 PI Van Den Brink EN;
 XX
 XX WPI; 2005-162947/17.
 XX
 XX New antigenic peptides from severe acute respiratory syndrome-coronavirus
 PT (SARS-CoV), useful in preparing a composition for diagnosing, treating or
 PT preventing SARS-CoV infection.
 XX
 XX Example 2; SEQ ID NO 582; 199pp; English.
 PS
 XX

CC The invention relates to an antigenic peptide from severe acute
 CC respiratory syndrome-coronavirus (SARS-CoV). The peptide or nucleic acid
 CC molecule encoding the peptide, fusion protein, conjugate or antibody is
 CC useful in preparing a composition for diagnosing, treating or preventing
 CC SARS-CoV infection. The present sequence represents a phage scFv SARS
 CC antibody.
 XX
 XX Sequence 247 AA;
 SQ
 Query Match 100.0%; Score 576; DB 9; Length 247;
 Best Local Similarity 100.0%; Pred. No. 7.1e-35;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 Qy 1 SELTQDPAVSVALGQTVRITTCQGSLSRSYASWTQKPGQAPVLVIYKNNRPSGIDPRF 60
 Db |||||
 Qy 137 SELTQDPAVSVALGQTVRITTCQGSLSRSYASWTQKPGQAPVLVIYKNNRPSGIDPRF 196
 Db |||||
 Qy 61 SGSSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGKTLTVLGAAA 111
 Db |||||
 Qy 197 SGSSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGKTLTVLGAAA 247
 Db |||||
 RESULT 9
 ID ADX01809 standard; protein; 247 AA.
 XX
 AC ADX01809;
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE SARS coronavirus scFv antibody SEQ ID NO 65.
 XX
 KW severe acute respiratory syndrome; diagnosis; Respiratory-Gen.; Virucide;
 KW respiratory disease; infection; antibody.
 XX
 OS SARS coronavirus.
 XX
 PN WO2005012360-A2.
 XX
 PD 10-FEB-2005.
 XX
 PF 21-JUL-2004; 2004WO-EP051568.
 XX
 PR 22-JUL-2003; 2003WO-EP050328.
 PR 01-SEP-2003; 2003WO-EP050391.
 PR 16-OCT-2003; 2003WO-EP050723.
 PR 24-NOV-2003; 2003WO-EP050883.
 PR 04-DEC-2003; 2003WO-EP050943.
 PR 13-FEB-2004; 2004WO-EP050127.
 PR 19-MAR-2004; 2004WO-EP050334.
 PR 07-APR-2004; 2004WO-EP050464.
 PR 14-APR-2004; 2004WO-EP050516.
 PR 29-APR-2004; 2004WO-EP050643.
 XX
 XX (CRUC-) CRUCCELL HOLLAND BV.
 XX
 XX Ter Meulen JH, De Kruif CA, Van Den Brink EN, Goudsmit J;
 PI WPI; 2005-142879/15.
 DR N-PSDB; ADX01808.
 XX
 XX New binding molecules that specifically bind to severe acute respiratory
 PT syndrome (SARS)-coronavirus (CoV), useful for diagnosing, preventing or
 PT treating conditions resulting from SARS-CoV.
 XX
 XX Example 3; SEQ ID NO 65; 633pp; English.
 XX
 XX The invention relates to a binding molecule, or its variant, capable of
 CC specifically binding to a severe acute respiratory syndrome (SARS)-
 CC coronavirus (CoV). The composition (including the binding molecule or its
 CC functional variant, or the immunoconjugate) is useful as a medicament for
 CC the diagnosis, prophylaxis or treatment of a condition resulting from a
 CC the diagnosis, prophylaxis or treatment of a condition resulting from a

CC SARS-CoV, or in the preparation of the medicament. The present sequence
 CC represents a SARS coronavirus scFv.
 XX
 SQ Sequence 247 AA;

Query Match 100.0%; Score 576; DB 9; Length 247;
 Best Local Similarity 100.0%; Pred. No. 7.1e-35;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTQDPVAVSVALGQTVRITTCQGDLSRSYASWYQKPGQAPVLVIYGNRPSGIDPRF 60
 |||||
 DB 137 SELTQDPVAVSVALGQTVRITTCQGDLSRSYASWYQKPGQAPVLVIYGNRPSGIDPRF 196
 |||||

QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFVGGTGLTVLGAAA 111
 |||||
 DB 197 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFVGGTGLTVLGAAA 247
 |||||

RESULT 10
 ADR23324
 ID ADR23324 standard; protein; 249 AA.
 XX
 AC ADR23324;
 XX
 DT 04-NOV-2004 (first entry)
 XX
 DE Human CD72-targeted scFv Sc02-025.
 XX
 KW Human; CD72; B-lymphocyte; receptor; scFv; antibody; cytostatic;
 KW immunosuppressive; cancer; autoimmune disease; gene therapy.
 XX
 OS Synthetic.
 XX

Key Location/Qualifiers
 FT Region 101..112
 FT /label= CDR3
 PN WO2004067569-A1.
 XX
 PD 12-AUG-2004.
 XX
 PF 27-JAN-2003; 2003WO-EP050004.
 XX
 PR 27-JAN-2003; 2003WO-EP050004.
 XX
 PA (CRUC-) CRUCCELL HOLLAND BV.
 XX
 PI Bakker ABH, Marissen WE;
 XX
 PI WPI; 2004-580978/56.
 DR
 DR N-PSDB; ADR23323.
 XX

New internalizing human binding molecules capable of specifically binding
 to CD72, useful for diagnosing and/or treating B-cell associated
 diseases, such as cancer or autoimmune disorders.
 XX
 PS Example 3; SEQ ID NO 16; 174pp; English.
 XX

The present sequence is the protein sequence of Sc02-025, an scFv that
 specifically recognises human B cell associated antigen CD72. It
 comprises V_H Dp07 and V_HII germline sequences. The scFv was selected
 from an antibody phage display library using human tonsillar mononuclear
 cells as target. It was shown to selectively bind to peripheral blood
 CD19+ B cells and to CD72-transfected U937 cells. Plasmid DNA was
 obtained from the scFv clone and used to determine the scFv nucleic acid
 and amino acid sequences. Sc02-025 scFv was used to generate CD72-
 directed human IgG1 antibodies comprising heavy chain ADR23350 and light
 chain ADR23362 sequences. Such anti-CD72 immunoglobulins or their antigen
 -binding fragments can be used as internalising human binding molecules
 of the invention. These internalising human binding molecules are capable
 of (specifically) binding to CD72 or its antigenic determinant, and
 CC preferably bind to CD72 associated with cells. Upon binding to CD72
 CC present on the surface of target cells, the binding molecules

CC internalise. In addition to the internalising human binding molecules,
 CC the invention provides immunoconjugates comprising an internalising human
 CC binding molecule and a tag (toxic substance, radioactive substance,
 CC liposome and/or enzyme), nucleic acids encoding these, and compositions
 CC comprising them. The internalising human binding molecule,
 CC immunoconjugate, nucleic acid molecule or composition can be used in the
 CC diagnosis and/or treatment of a B cell associated disorder or disease,
 CC especially a B cell associated cancer and B cell associated autoimmune
 CC disorder (claimed).
 XX
 SQ Sequence 249 AA;

Query Match 100.0%; Score 576; DB 8; Length 249;
 Best Local Similarity 100.0%; Pred. No. 7.1e-35;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTQDPVAVSVALGQTVRITTCQGDLSRSYASWYQKPGQAPVLVIYGNRPSGIDPRF 60
 |||||
 DB 139 SELTQDPVAVSVALGQTVRITTCQGDLSRSYASWYQKPGQAPVLVIYGNRPSGIDPRF 198
 |||||

QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFVGGTGLTVLGAAA 111
 |||||
 DB 199 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFVGGTGLTVLGAAA 249
 |||||

RESULT 11
 ADR23323
 ID ADR23323 standard; protein; 260 AA.
 XX
 AC ADR23323;
 XX
 DT 04-DEC-2002 (first entry)
 XX
 DE Antibody protein #3.
 XX
 DE Antibody; epitope; cancer; tumour; cell rolling; inflammation;
 KW metastasis; hypervariable region; autoimmune disease; thrombosis;
 KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
 KW myocardial infarction; retinopathic disease; abnormal platelet function;
 KW sulphated tyrosine-dependent protein-protein interaction.
 XX
 OS Unidentified.
 XX
 PN WO200253700-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 31-DEC-2001; 2001WO-US049442.
 XX
 PR 29-DEC-2000; 2000US-00751181.
 PR 29-DEC-2000; 2000US-0258948P.
 XX
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
 XX
 PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
 PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
 XX
 WIPI; 2002-674776/72.
 XX

Novel isolated epitope present on cancer cells and important in
 PT physiological phenomena such as cell rolling, metastasis and
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular
 PT diseases, and cancer.
 XX
 PS Disclosure; Fig 49; Opp; English.
 XX

The invention relates to an isolated epitope present on cancer cells and
 CC important in physiological phenomena such as cell rolling, metastasis and
 CC inflammation, where the epitope is capable of being bound by an antibody,
 CC its antigen-binding fragment or its complex comprising at least one
 CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of

CC tumour or leukaemia cells, increase in number of tumour or leukaemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia
 CC cells in a patient, or in the manufacture of a medicament for the above
 CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents an antibody protein of the
 CC invention
 XX
 SQ Sequence 260 AA;

Query Match 100.0%; Score 576; DB 5; Length 260;
 Best Local Similarity 100.0%; Pred. No. 7.4e-35;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTQDPANVSVALGQTVRITTCQGSLSRSYASWYQKPGQAPVLVIYKNNRPSGIDPRF 60
 DB 136 SELTQDPANVSVALGQTVRITTCQGSLSRSYASWYQKPGQAPVLVIYKNNRPSGIDPRF 195
 QY 61 SGSSSGNTASLTITGAQAEADYCNRSRDSGNHVVFGGTKLTVLGAAA 111
 DB 196 SGSSSGNTASLTITGAQAEADYCNRSRDSGNHVVFGGTKLTVLGAAA 246

RESULT 12

ABG92024
 ID ABG92024 standard; protein; 263 AA.

AC ABG92024;

XX 04-DEC-2002 (first entry)

XX Antibody protein #4.

XX Antibody; epitope; cancer; tumour; cell rolling; inflammation;
 KW metastasis; hypervariable region; autoimmune disease; thrombosis;
 KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
 KW myocardial infarction; retinopathic disease; abnormal platelet function;
 KW sulphated tyrosine-dependent protein-protein interaction.

XX Unidentified.

XX WO200253700-A2.

XX 11-JUL-2002.

XX 31-DEC-2001; 2001WO-US049442.

XX 29-DEC-2000; 2000US-00751181.

XX 29-DEC-2000; 2000US-0258948P.

XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
 PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
 XX WPI; 2002-674776/72.

XX Novel isolated epitope present on cancer cells and important in
 PT physiological phenomena such as cell rolling, metastasis and
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular
 PT diseases, and cancer.

XX Disclosure; Fig 50; Opp; English.

XX The invention relates to an isolated epitope present on cancer cells and
 CC important in physiological phenomena such as cell rolling, metastasis and

CC inflammation, where the epitope is capable of being bound by an antibody,
 CC its antigen-binding fragment or its complex comprising at least one
 CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia
 CC cells in a patient, or in the manufacture of a medicament for the above
 CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents an antibody protein of the
 CC invention
 XX

SQ Sequence 263 AA;

Query Match 100.0%; Score 576; DB 5; Length 263;
 Best Local Similarity 100.0%; Pred. No. 7.5e-35;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTQDPANVSVALGQTVRITTCQGSLSRSYASWYQKPGQAPVLVIYKNNRPSGIDPRF 60
 DB 133 SELTQDPANVSVALGQTVRITTCQGSLSRSYASWYQKPGQAPVLVIYKNNRPSGIDPRF 192
 QY 61 SGSSSGNTASLTITGAQAEADYCNRSRDSGNHVVFGGTKLTVLGAAA 111
 DB 193 SGSSSGNTASLTITGAQAEADYCNRSRDSGNHVVFGGTKLTVLGAAA 243

RESULT 13

ABG92020
 ID ABG92020 standard; protein; 266 AA.

XX AC ABG92020;

XX 04-DEC-2002 (first entry)

XX Human antibody fragment #204.

XX Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
 KW metastasis; hypervariable region; autoimmune disease; thrombosis;
 KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
 KW myocardial infarction; retinopathic disease; abnormal platelet function;
 KW sulphated tyrosine-dependent protein-protein interaction.

XX Homo sapiens.

XX WO200253700-A2.

XX 11-JUL-2002.

XX 31-DEC-2001; 2001WO-US049442.

XX 29-DEC-2000; 2000US-00751181.

XX 29-DEC-2000; 2000US-0258948P.

XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
 PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
 XX WPI; 2002-674776/72.

XX Novel isolated epitope present on cancer cells and important in
 PT physiological phenomena such as cell rolling, metastasis and
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular
 PT diseases, and cancer.

XX PS Disclosure; Page 309-310; Opp; English.

XX CC The invention relates to an isolated epitope present on cancer cells and

XX CC important in physiological phenomena such as cell rolling, metastasis and

XX CC inflammation, where the epitope is capable of being bound by an antibody,

XX CC its antigen-binding fragment or its complex comprising at least one

XX CC antibody or its binding fragment having a first hypervariable region. The

XX CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune

XX CC disease, thrombosis, restenosis, metastasis, growth and/or replication of

XX CC tumour or leukaemia cells, increase in number of tumour or leukaemia

XX CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-

XX CC platelet and/or cell-platelet adhesion or aggregation, for increasing

XX CC mortality of tumour or leukaemia cells, for increasing the susceptibility

XX CC of diseased cells to damage by anti-disease, anti-cancer or anti-

XX CC leukaemia agents, or for decreasing the number of tumour or leukaemia

XX CC cells in a patient, or in the manufacture of a medicament for the above

XX CC mentioned purposes. The epitopes are useful for diagnosing and treating

XX CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory

XX CC diseases, cardiovascular diseases such as myocardial infarction,

XX CC retinopathic diseases and other diseases mediated by abnormal platelet

XX CC function and diseases caused by sulphated tyrosine-dependent protein-

XX CC protein interactions. This sequence represents a human antibody fragment

XX CC of the invention

XX SQ Sequence 266 AA;

Query Match 100.0%; Score 576; DB 5; Length 266;

Best Local Similarity 100.0%; Pred. No. 7.6e-35;

Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTQDPAVSVLGGTQVTRITCGDLSRSYASWYQKPGQAPVLVIYGNRRSGIPDRF 60

DB 153 SELTQDPAVSVLGGTQVTRITCGDLSRSYASWYQKPGQAPVLVIYGNRRSGIPDRF 212

QY 61 SGSSSGNTASLTITGAQDEADYCNRSRDSGNHVVFGGTKLTVLGAAA 111

DB 213 SGSSSGNTASLTITGAQDEADYCNRSRDSGNHVVFGGTKLTVLGAAA 263

RESULT 14

ABG78150

ID ABG78150 standard; protein; 277 AA.

XX AC ABG78150;

XX DT 15-NOV-2002 (first entry)

XX DE Human Fv molecule hypervariable region related peptide #25.

XX KW Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;

XX KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;

XX KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.

XX OS Homo sapiens.

XX PN WO200259264-A2.

XX PD 01-AUG-2002.

XX PF 31-DEC-2001; 2001WO-US049440.

XX PR 29-DEC-2000; 2000US-00751181.

XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;

XX PI Plaksin D, Peretz T;

XX DR WPI; 2002-619166/66.

XX PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct

XX PT or fragment, or construct of fragment with enhanced binding

XX PT characteristics so as to selectively bind target cell in favor of other

XX PT cells.

XX PT

XX PT characteristics so as to selectively bind target cell in favor of other

XX PT cells.

XX Claim 4; Page 155-156; 232pp; English.

XX CC The invention relates to a peptide or polypeptide comprising an Fv

XX CC molecule, a construct or fragments or a construct of a fragment with

XX CC enhanced binding characteristics which selectively and/or specifically

XX CC binds to a target cell in favour of other cells, where binding is

XX CC primarily determined by a first hypervariable region and Fv is a single

XX CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in

XX CC association with or attached, coupled, combined, linked or fused to a

XX CC pharmaceutical agent, is useful in the manufacture of a medicament, where

XX CC the medicament has activity against a diseased cell, preferably a cancer

XX CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,

XX CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an

XX CC acute myeloid leukaemia cell). The peptide is also useful for preparing a

XX CC composition for use in inhibiting the growth of a diseased or cancer

XX CC cell. This sequence represents a human Fv molecule hypervariable region

XX CC related peptide of the invention

XX SQ Sequence 277 AA;

Query Match 100.0%; Score 576; DB 5; Length 277;

Best Local Similarity 100.0%; Pred. No. 7.9e-35;

Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTQDPAVSVLGGTQVTRITCGDLSRSYASWYQKPGQAPVLVIYGNRRSGIPDRF 60

DB 153 SELTQDPAVSVLGGTQVTRITCGDLSRSYASWYQKPGQAPVLVIYGNRRSGIPDRF 212

QY 61 SGSSSGNTASLTITGAQDEADYCNRSRDSGNHVVFGGTKLTVLGAAA 111

DB 213 SGSSSGNTASLTITGAQDEADYCNRSRDSGNHVVFGGTKLTVLGAAA 263

RESULT 15

ABG78328

ID ABG78328 standard; protein; 277 AA.

XX AC ABG78328;

XX DT 15-NOV-2002 (first entry)

XX DE Human Fv molecule hypervariable region related peptide #203.

XX KW Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;

XX KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;

XX KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.

XX OS Homo sapiens.

XX PN WO200259264-A2.

XX PD 01-AUG-2002.

XX PF 31-DEC-2001; 2001WO-US049440.

XX PR 29-DEC-2000; 2000US-00751181.

XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;

XX PI Plaksin D, Peretz T;

XX DR WPI; 2002-619166/66.

XX DR N-PSDB; AB863384.

XX PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct

XX PT or fragment, or construct of fragment with enhanced binding

XX PT characteristics so as to selectively bind target cell in favor of other

XX PT cells.

PS Claim 141; Fig 14; 232pp; English.

XX The invention relates to a peptide or polypeptide comprising an Fv
CC molecule, a construct or fragments or a construct of a fragment with
CC enhanced binding characteristics which selectively and/or specifically
CC binds to a target cell in favour of other cells, where binding is
CC primarily determined by a first hypervariable region and Fv is a single
CC chain Fv (FcFv) or a disulfide Fv (dsFv). The peptide, optionally in
CC association with or attached, coupled, combined, linked or fused to a
CC pharmaceutical agent, is useful in the manufacture of a medicament, where
CC the medicament has activity against a diseased cell, preferably a cancer
CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
CC composition for use in inhibiting the growth of a diseased or cancer
CC cell. This sequence represents a human Fv molecule hypervariable region
CC related peptide of the invention

XX Sequence 277 AA;

Query Match 100.0%; Score 576; DB 5; Length 277;
Best Local Similarity 100.0%; Pred. No. 7.9e-35;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SELTQDPAVSVALGQTVRITCGDSLSRSYYASWYQKPGQAPVLVIYGNRPSGIPDRF 60
Db 153 SELTQDPAVSVALGQTVRITCGDSLSRSYYASWYQKPGQAPVLVIYGNRPSGIPDRF 212
Qy 61 SGSSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGKLTVLGAAA 111
Db 213 SGSSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGKLTVLGAAA 263

Search completed: November 18, 2005, 21:46:15
Job time : 64.6278 secs

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OM protein - protein search, using sw model

Run on: November 18, 2005, 21:40:23 ; Search time 15.2319 Seconds
(without alignments)
602.487 Million cell updates/sec

Title: US-10-029-926D-7
Perfect score: 576
Sequence: 1 SELTQDPAVSVALGQTVRIT.....SGNHVFGGKTGLTVLGAAA 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/ptodata/1/1aa/H-COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/PCITUS-COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/RE-COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	576	100.0	278	2	US-09-260-527-3
2	576	100.0	280	2	US-09-260-527-1
3	576	100.0	309	2	US-09-079-029-9
4	576	100.0	312	2	US-09-079-029-10
5	558	96.9	108	2	US-09-720-493-4
6	554	96.2	111	2	US-09-203-768A-8
7	537	92.2	109	1	US-08-652-816A-16
8	531.5	92.3	109	1	US-08-665-202-34
9	531.5	92.3	109	2	US-09-315-574-34
10	525	91.1	101	2	US-09-726-219A-168
11	525	91.1	101	2	US-09-196-522-168
12	502	87.2	97	1	US-08-665-202-35
13	502	87.2	97	2	US-08-315-574-35
14	494.5	85.9	104	2	US-08-793-450-2
15	494.5	85.9	238	2	US-08-793-450-6
16	487	84.5	104	2	US-09-240-274-49
17	487	84.5	104	2	US-09-848-798-49
18	480	83.3	106	2	US-09-240-274-48
19	480	83.3	106	2	US-09-848-798-48
20	475.5	82.6	102	2	US-09-726-219A-174
21	475.5	82.6	102	2	US-09-196-522-174
22	473	82.1	106	2	US-09-240-274-47
23	473	82.1	106	2	US-09-240-274-50
24	473	82.1	106	2	US-09-848-798-47
25	473	82.1	106	2	US-09-848-798-50
26	471	81.8	103	1	US-08-273-146-71
27	448.5	77.9	108	2	US-09-025-769B-20

28	448.5	77.9	108	2	US-09-490-070A-20
29	448.5	77.9	108	2	US-09-490-153-20
30	448.5	77.9	108	2	US-09-490-324-20
31	443.5	77.0	105	1	US-08-488-113B-157
32	443.5	77.0	105	1	US-08-477-484B-157
33	443.5	77.0	105	1	US-08-107-669D-21
34	443.5	77.0	105	1	US-08-472-788A-21
35	443.5	77.0	105	1	US-08-477-531B-21
36	443.5	77.0	105	1	US-08-646-360-157
37	443.5	77.0	105	1	US-08-082-842A-21
38	443.5	77.0	105	2	US-08-839-765-157
39	443.5	77.0	105	2	US-09-136-389-157
40	443.5	77.0	105	2	US-09-610-838-157
41	443.5	77.0	105	2	US-09-711-485-157
42	441	76.6	125	2	US-09-471-276-1249
43	423	73.4	108	1	US-08-360-125-12
44	423	73.4	108	1	US-08-450-578-12
45	423	73.4	108	1	US-09-017-628-12

ALIGNMENTS

RESULT 1

US-09-260-527-3
; Sequence 3, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
; APPLICANT: Knox, J.P.
; APPLICANT: Mikkelsen, J.D.
; APPLICANT: Willats, W. G.
; TITLE OF INVENTION: ANTIBODY
; FILE REFERENCE: DY0U19.001AUS
; CURRENT APPLICATION NUMBER: US/09/260.527A
; CURRENT FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 278
; TYPE: PRT
; ORGANISM: UNKNOWN
; FEATURE:
; OTHER INFORMATION: Anti-homogalacturonan specific antibodies selected from a naive phage display library known as the
; OTHER INFORMATION: Synthetic scFv Library (#1) from the Centre for
; OTHER INFORMATION: Protein Engineering, MRC Centre, Cambridge, UK
US-09-260-527-3

Query Match 100.0%; Score 576; DB 2; Length 278;
Best Local Similarity 100.0%; Pred. No. 1.6e-47;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	SELTQDPAVSVALGQTVRITCGDLSRSYASVYQQKPGQAPVLIYGNRPSGIDPRF 60
Db	154	SELTQDPAVSVALGQTVRITCGDLSRSYASVYQQKPGQAPVLIYGNRPSGIDPRF 213
Qy	61	SGSSSGNTASLTITGAQAEADYCNRSRDSNGHVFGGKTGLTVLGAAA 111
Db	214	SGSSSGNTASLTITGAQAEADYCNRSRDSNGHVFGGKTGLTVLGAAA 264

RESULT 2

US-09-260-527-1
; Sequence 1, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
; APPLICANT: Knox, J.P.
; APPLICANT: Mikkelsen, J.D.
; APPLICANT: Willats, W. G.
; TITLE OF INVENTION: ANTIBODY
; FILE REFERENCE: DY0U19.001AUS
; CURRENT APPLICATION NUMBER: US/09/260.527A
; CURRENT FILING DATE: 1999-02-26

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; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 280
; TYPE: PRT
; ORGANISM: UNKNOWN
; FEATURE:
; OTHER INFORMATION: Anti-homogalacturonan specific antibodies from a
; OTHER INFORMATION: phage display library known as the Synthetic scFv
; OTHER INFORMATION: Library (#1) from the Centre for Protein
; OTHER INFORMATION: Engineering, MRC Centre, Cambridge, UK.
US-09-260-527-1

Query Match          100.0%; Score 576; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 1.8e-47;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTQDPAVSVAGQTVRITTCQGDSLSYASWYQKPGQAPVLVIYGNRRSGIPDRF 60
Db 156 SELTQDPAVSVAGQTVRITTCQGDSLSYASWYQKPGQAPVLVIYGNRRSGIPDRF 215

QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTTKLTVLGAAA 111
Db 216 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTTKLTVLGAAA 266

RESULT 3
US-09-079-029-9
; Sequence 9, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-079-029-9

Query Match          100.0%; Score 576; DB 2; Length 309;
Best Local Similarity 100.0%; Pred. No. 1.8e-47;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTQDPAVSVAGQTVRITTCQGDSLSYASWYQKPGQAPVLVIYGNRRSGIPDRF 60
Db 156 SELTQDPAVSVAGQTVRITTCQGDSLSYASWYQKPGQAPVLVIYGNRRSGIPDRF 215

QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTTKLTVLGAAA 111
Db 216 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTTKLTVLGAAA 266

RESULT 4
US-09-079-029-10
; Sequence 10, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-079-029-10

Query Match          100.0%; Score 576; DB 2; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.8e-47;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTQDPAVSVAGQTVRITTCQGDSLSYASWYQKPGQAPVLVIYGNRRSGIPDRF 60
Db 179 SELTQDPAVSVAGQTVRITTCQGDSLSYASWYQKPGQAPVLVIYGNRRSGIPDRF 238

QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTTKLTVLGAAA 111
Db 239 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTTKLTVLGAAA 289

RESULT 5
US-09-720-493-4
; Sequence 4, Application US/09720493
; Patent No. 6827925
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Williams, Andrew J
; APPLICANT: Tempest, Philip R
; APPLICANT: Holtet, Thor L
; APPLICANT: Main, Sarah H
; APPLICANT: Jackson, Helen
; APPLICANT: Daramola, Olalekan
```

```
Db 176 SELTQDPAVSVAGQTVRITTCQGDSLSYASWYQKPGQAPVLVIYGNRRSGIPDRF 235

QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTTKLTVLGAAA 111
Db 236 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTTKLTVLGAAA 286

RESULT 4
US-09-079-029-10
; Sequence 10, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-079-029-10

Query Match          100.0%; Score 576; DB 2; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.8e-47;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTQDPAVSVAGQTVRITTCQGDSLSYASWYQKPGQAPVLVIYGNRRSGIPDRF 60
Db 179 SELTQDPAVSVAGQTVRITTCQGDSLSYASWYQKPGQAPVLVIYGNRRSGIPDRF 238

QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTTKLTVLGAAA 111
Db 239 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTTKLTVLGAAA 289

RESULT 5
US-09-720-493-4
; Sequence 4, Application US/09720493
; Patent No. 6827925
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Williams, Andrew J
; APPLICANT: Tempest, Philip R
; APPLICANT: Holtet, Thor L
; APPLICANT: Main, Sarah H
; APPLICANT: Jackson, Helen
; APPLICANT: Daramola, Olalekan
```



```
; TITLE OF INVENTION: Improvements relating to antibodies
; FILE REFERENCE: AHE/CP5775333
; CURRENT APPLICATION NUMBER: US/09/720,493
; CURRENT FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: GB 9814383.7
; PRIOR FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-720-493-4

Query Match          96.9%; Score 558; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.8e-46;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELTQDPAVSVALGQTVRITTCQGSLSRSYYASWYQKFGQAPVLVIYGNRPSPGIDPRF 60
Db 2 SELTQDPAVSVALGQTVRITTCQGSLSRSYYASWYQKFGQAPVLVIYGNRPSPGIDPRF 61

Qy 61 SGSSSGNTASLTITGAQAEADYIYCNRSRDSGNHVVFGGTKLTVL 107
Db 62 SGSSSGNTASLTITGAQAEADYIYCNRSRDSGNHVVFGGTKLTVL 108

RESULT 6
US-09-203-768A-8
; Sequence 8, Application US/09203768A
; Patent No. 6787638
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Tumor Specific Human Monoclonal Antibodies and Methods
; TITLE OF INVENTION: of Use
; FILE REFERENCE: P-IX 2947
; CURRENT APPLICATION NUMBER: US/09/203,768A
; CURRENT FILING DATE: 1998-12-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-203-768A-8

Query Match          96.2%; Score 554; DB 2; Length 111;
Best Local Similarity 99.1%; Pred. No. 7e-46;
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SELTQDPAVSVALGQTVRITTCQGSLSRSYYASWYQKFGQAPVLVIYGNRPSPGIDPRF 60
Db 2 SELTQDPAVSVALGQTVRITTCQGSLSRSYYASWYQKFGQAPVLVIYGNRPSPGIDPRF 61

Qy 61 SGSSSGNTASLTITGAQAEADYIYCNRSRDSGNHVVFGGTKLTVLG 108
Db 62 SGSSSGNTASLTITGAQAEADYIYCNRSRDSGNHVVFGGTKLTVLG 109

RESULT 7
US-08-652-816A-16
; Sequence 16, Application US/08652816A
; Patent No. 5872215
; GENERAL INFORMATION:
; APPLICANT: Osbourn, JK
; APPLICANT: Allen, DJ
; APPLICANT: McCafferty, JG
; TITLE OF INVENTION: Specific binding members, materials and
; TITLE OF INVENTION: methods.
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; TITLE OF INVENTION: Improvements relating to antibodies
; FILE REFERENCE: AHE/CP5775333
; CURRENT APPLICATION NUMBER: US/09/720,493
; CURRENT FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: GB 9814383.7
; PRIOR FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-720-493-4

STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,816A
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525004.9
FILING DATE: 07-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/02240
FILING DATE: 02-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/244,597
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/33308
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-652-816A-16

Query Match          93.2%; Score 537; DB 1; Length 109;
Best Local Similarity 96.2%; Pred. No. 2.9e-44;
Matches 102; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SELTQDPAVSVALGQTVRITTCQGSLSRSYYASWYQKFGQAPVLVIYGNRPSPGIDPRF 60
Db 2 SELTQDPAVSVALGQTVRITTCQGSLSRSYYASWYQKFGQAPVLVIYGNRPSPGIDPRF 61

Qy 61 SGSSSGNTASLTITGAQAEADYIYCNRSRDSGNHVVFGGTKLTV 106
Db 62 SGSSSGNTASLTITGAQAEADYIYCNRSRDSGNHVVFGGTKLEI 107

RESULT 8
US-08-665-202-34
; Sequence 34, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
```

```

; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,202
; FILING DATE: 13-JUN-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061410
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-665-202-34

Query Match 92.3%; Score 531.5; DB 1; Length 109;
Best Local Similarity 95.4%; Pred. No. 9.8e-44;
Matches 104; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 SELTQDPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLVIYKKNRPSGIPDRF 60
Db 1 SELTQDPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLVIYKKNRPSGIPDRF 60

QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGN-HVVFGGGKTLTVLG 108
Db 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNPYWVFGGKTKTVLG 109

RESULT 9
US-09-315-574-34
; Sequence 34, Application US/09315574
; Patent No. 6512097
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
; STREET: Four Embarcadero Center, Suite 1100
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4106
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/315,574
; FILING DATE: 20-MAY-99
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/665,202
; FILING DATE: 13-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061411
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-315-574-34

Query Match 92.3%; Score 531.5; DB 2; Length 109;
Best Local Similarity 95.4%; Pred. No. 9.8e-44;
Matches 104; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 SELTQDPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLVIYKKNRPSGIPDRF 60
Db 1 SELTQDPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLVIYKKNRPSGIPDRF 60

QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGN-HVVFGGGKTLTVLG 108
Db 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNPYWVFGGKTKTVLG 109

RESULT 10
US-09-726-219A-168
; Sequence 168, Application US/09726219A
; Patent No. 6806079
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Grifiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 213839-00013
; CURRENT APPLICATION NUMBER: US/09/726,219A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12

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; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 168
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-726-219A-168

Query Match          91.1%; Score 525; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 3.7e-43;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELTQDPAVSVALGQTVRIITCGDSLRSYASWYQKPGQAPVLVIYKNNRPSGIDPRF 60
   |||||||
Db 2 SELTQDPAVSVALGQTVRIITCGDSLRSYASWYQKPGQAPVLVIYKNNRPSGIDPRF 61
   |||||||

Qy 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGG 100
   |||||||
Db 62 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGG 101
   |||||||

RESULT 11
US-09-196-522-168
; Sequence 168, Application US/09196522
; Patent No. 6916605
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 213839-00004
; CURRENT APPLICATION NUMBER: US/09/196,522
; CURRENT FILING DATE: 1998-11-28
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07

; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 168
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-726-219A-168

Query Match          91.1%; Score 525; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 3.7e-43;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELTQDPAVSVALGQTVRIITCGDSLRSYASWYQKPGQAPVLVIYKNNRPSGIDPRF 60
   |||||||
Db 2 SELTQDPAVSVALGQTVRIITCGDSLRSYASWYQKPGQAPVLVIYKNNRPSGIDPRF 61
   |||||||

Qy 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGG 100
   |||||||
Db 62 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGG 101
   |||||||

RESULT 12
US-08-665-202-35
; Sequence 35, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to
; Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,202
; FILING DATE: 13-JUN-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061410
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 97 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-665-202-35

Query Match          87.2%; Score 502; DB 1; Length 97;
Best Local Similarity 99.0%; Pred. No. 5.7e-41;
Matches 96; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 SELTQDPAVSVALGQTVRITTCQDGLSLRSYASWYQKPGQAPVLVIYGNRRPSGIDPRF 60
 Db 1 SSSLTQDPAVSVALGQTVRITTCQDGLSLRSYASWYQKPGQAPVLVIYGNRRPSGIDPRF 60
 Qy 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVV 97
 Db 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVV 97

RESULT 13

US-09-315-574-35
 ; Sequence 35, Application US/09315574
 ; Patent No. 6512097
 ; GENERAL INFORMATION:
 ; APPLICANT: Marks, James D.
 ; APPLICANT: Schier, Robert
 ; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
 ; TITLE OF INVENTION: Tumor Antigens
 ; NUMBER OF SEQUENCES: 141
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Majestic, Parsons, Siebert & Heue P.C.
 ; STREET: Four Embarcadero Center, Suite 1100
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-4106
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/315,574
 ; FILING DATE: 20-MAY-99
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/000,238
 ; FILING DATE: 14-JUN-1995
 ; APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/000,250
 ; FILING DATE: 15-JUN-1995
 ; APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/665,202
 ; FILING DATE: 13-JUN-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hunter, Tom
 ; REGISTRATION NUMBER: 38,498
 ; REFERENCE/DOCKET NUMBER: 02307E-061411
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 35:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 97 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-09-315-574-35

Query Match 87.2%; Score 502; DB 2; Length 97;
 Best Local Similarity 99.0%; Pred. No. 5.7e-41;
 Matches 96; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 SELTQDPAVSVALGQTVRITTCQDGLSLRSYASWYQKPGQAPVLVIYGNRRPSGIDPRF 60
 Db 1 SSSLTQDPAVSVALGQTVRITTCQDGLSLRSYASWYQKPGQAPVLVIYGNRRPSGIDPRF 60
 Qy 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVV 97
 Db 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVV 97

RESULT 14

US-08-793-450-2
 ; Sequence 2, Application US/08793450
 ; Patent No. 6312690
 ; GENERAL INFORMATION:
 ; APPLICANT: EDELMAN, LENA
 ; APPLICANT: MARGARITTE, CHRISTEL
 ; APPLICANT: KACZOREK, MICHEL
 ; APPLICANT: CHAABIHI, HASSAN
 ; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
 ; TITLE OF INVENTION:
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 ; ADDRESSEE: P.C.
 ; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
 ; CITY: ARLINGTON
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/793,450
 ; FILING DATE: 03-MAR-1997
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: FR 94/10566
 ; FILING DATE: 02-SEP-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: OBLON, NORMAN F.
 ; REGISTRATION NUMBER: 24,618
 ; REFERENCE/DOCKET NUMBER: 660-118-0 PCT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-413-3000
 ; TELEFAX: 703-413-2220
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 104 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-793-450-2

Query Match 85.9%; Score 494.5; DB 2; Length 104;
 Best Local Similarity 90.7%; Pred. No. 3.2e-40;
 Matches 97; Conservative 2; Mismatches 3; Indels 5; Gaps 1;
 Qy 2 ELTQDPAVSVALGQTVRITTCQDGLSLRSYASWYQKPGQAPVLVIYGNRRPSGIDPRF 61
 Db 3 ELTQDPAVSVALGQTVRITTCQDGLSLRSYASWYQKPGQAPVLVIYGNRRPSGIDPRF 62
 Qy 62 GSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGKTLTVLG 108
 Db 63 GSSSGNTASLTITGAQAEADYYCNSGGK-----VFGGKTLTVLG 104

RESULT 15

US-08-793-450-6
 ; Sequence 6, Application US/08793450
 ; Patent No. 6312690
 ; GENERAL INFORMATION:
 ; APPLICANT: EDELMAN, LENA
 ; APPLICANT: MARGARITTE, CHRISTEL
 ; APPLICANT: KACZOREK, MICHEL
 ; APPLICANT: CHAABIHI, HASSAN
 ; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
 ; TITLE OF INVENTION:
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;; ADDRESSEE: P.C.
;; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
;; CITY: ARLINGTON
;; STATE: VA
;; COUNTRY: USA
;; ZIP: 22202
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/793,450
;; FILING DATE: 03-MAR-1997
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: FR 94/10566
;; FILING DATE: 02-SEP-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: OBLON, NORMAN F.
;; REGISTRATION NUMBER: 24,618
;; REFERENCE/DOCKET NUMBER: 680-118-0 PCT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 703-413-3000
;; TELEFAX: 703-413-2220
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 238 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-793-450-6

Query Match 85.9%; Score 494.5; DB 2; Length 238;
Best Local Similarity 90.7%; Pred. No. 8.3e-40;
Matches 97; Conservative 2; Mismatches 3; Indels 5; Gaps 1;
Qy 2 ELTQDPVSVVALGQTVRTTCGDSLSRYASWYQKPGQAPVLVIYGNRPSPGIPDRFS 61
Db 22 ELTQDPVSVVALGQTVRTTCGDSLSRYASWYQKPGQAPVLVIYGNRPSPGIPDRFS 81
Qy 62 GSSSGNTASLTITGAQAEDEADYYCNSRDSNGNHVFGGGTKLTVLG 108
Db 82 GSSSGNTASLTITGAQAEDEADYYCNSRDSNGNHVFGGGTKLTVLG 123

Search completed: November 18, 2005, 21:55:04
Job time : 17.2319 secs

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Result No.	Score	Query #		Length	DB	ID	Description
		Match					
1	576	100.0	111	15	US-10-032-037B-7		Sequence 7, Appli
2	576	100.0	111	15	US-10-029-988B-7		Sequence 7, Appli
3	576	100.0	111	15	US-10-032-423A-7		Sequence 7, Appli
4	576	100.0	111	15	US-10-028-926B-7		Sequence 7, Appli
5	576	100.0	125	17	US-10-888-959-8		Sequence 8, Appli
6	576	100.0	266	15	US-10-032-037B-204		Sequence 204, App
7	576	100.0	266	15	US-10-029-988B-204		Sequence 204, App
8	576	100.0	266	15	US-10-032-423A-204		Sequence 204, App
9	576	100.0	277	15	US-10-032-037B-25		Sequence 25, Appli
10	576	100.0	277	15	US-10-032-037B-203		Sequence 203, App
11	576	100.0	277	15	US-10-029-988B-25		Sequence 25, Appli
12	576	100.0	277	15	US-10-029-988B-203		Sequence 203, App
13	576	100.0	277	15	US-10-032-423A-25		Sequence 25, Appli

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; Sequence 7, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-7

Query Match      100.0%; Score 576; DB 15; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.1e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELTQDPAVSVALGQTVRITTCQGDSLSRSYASMTQKPGQAPVLVIYKKNRPSGIPDRF 60
Db 1 SELTQDPAVSVALGQTVRITTCQGDSLSRSYASMTQKPGQAPVLVIYKKNRPSGIPDRF 60

Qy 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTTKLTVLGAAA 111
Db 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTTKLTVLGAAA 111

RESULT 3
US-10-032-423A-7
; Sequence 7, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-7

Query Match      100.0%; Score 576; DB 15; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.1e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELTQDPAVSVALGQTVRITTCQGDSLSRSYASMTQKPGQAPVLVIYKKNRPSGIPDRF 60
Db 1 SELTQDPAVSVALGQTVRITTCQGDSLSRSYASMTQKPGQAPVLVIYKKNRPSGIPDRF 60

Qy 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTTKLTVLGAAA 111
Db 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTTKLTVLGAAA 111

RESULT 4
US-10-029-926B-7
; Sequence 7, Application US/10029926B
; Publication No. US20040073011A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
```

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; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-926B-7

Query Match      100.0%; Score 576; DB 15; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.1e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELTQDPAVSVALGQTVRITTCQGDSLSRSYASMTQKPGQAPVLVIYKKNRPSGIPDRF 60
Db 1 SELTQDPAVSVALGQTVRITTCQGDSLSRSYASMTQKPGQAPVLVIYKKNRPSGIPDRF 60

Qy 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTTKLTVLGAAA 111
Db 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTTKLTVLGAAA 111

RESULT 5
US-10-888-959-8
; Sequence 8, Application US/10888959
; Publication No. US20050048545A1
; GENERAL INFORMATION:
; APPLICANT: Cull, Millard
; APPLICANT: Brennan, Miles
; APPLICANT: Gill, Ronald
; TITLE OF INVENTION: Universal Detection of Binding
; FILE REFERENCE: BPP 03
; CURRENT APPLICATION NUMBER: US/10/888,959
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/487,018
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: US 60/509,196
; PRIOR FILING DATE: 2003-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: variable light chain domain
US-10-888-959-8

Query Match      100.0%; Score 576; DB 17; Length 125;
Best Local Similarity 100.0%; Pred. No. 3.5e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELTQDPAVSVALGQTVRITTCQGDSLSRSYASMTQKPGQAPVLVIYKKNRPSGIPDRF 60
Db 1 SELTQDPAVSVALGQTVRITTCQGDSLSRSYASMTQKPGQAPVLVIYKKNRPSGIPDRF 60

Qy 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTTKLTVLGAAA 111
Db 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTTKLTVLGAAA 111

RESULT 6
US-10-032-037B-204
; Sequence 204, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
```



```

; REFERENCE: BIOLOGY General Corp.
; TITLE OF INVENTION: Y11-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 277
; TYPE: PRT

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; ORGANISM: Homo sapiens
 US-10-032-037B-203

Query Match 100.0%; Score 576; DB 15; Length 277;
Best Local Similarity 100.0%; -Pred. NO. 8e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0

Qy		1 S E L T Q D P A V S V A L G Q T V R I T C Q G D S L R S Y Y A S W Y O K P G Q A P V L V I Y G K N R P S G I P D R F 60
Db		153 S E L T Q D P A V S V A L G Q T V R I T C Q G D S L R S Y Y A S W Y O K P G Q A P V L V I Y G K N R P S G I P D R F 212

[illegible]

RESULT 11
 US-10-029-988B-25
 ; Sequence 25, Application US/10029988B
 ; Publication No. US20040001839A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bio-Technology General Corp.
 ; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
 ; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF

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/ FILE REFERENCE: 10795/40
/ CURRENT APPLICATION NUMBER: US/10/029,988B
/ CURRENT FILING DATE: 2001-12-31
/ PRIOR APPLICATION NUMBER: 60/358,948
/ PRIOR FILING DATE: 2000-12-29
/ NUMBER OF SEQ ID NOS: 204
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 25
/ LENGTH: 277

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US-10-029-988B-25

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Best Local Similarity 100.0%; Pred. NO. 8e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEUTQDPAVSVALGQTVRITCOGDSLSRYASWYQKPGQAPVLVIYGNKRPSGIPDRF 60
Db 153 SEUTQDPAVSVALGQTVRITCOGDSLSRYASWYQKPGQAPVLVIYGNKRPSGIPDRF 212

QY 61 SGSSSGNTASLTITGAQAEADYVYCNRSRDSGNHVVFGGGTKLTVLAAA 111
Db 213 SGSSSGNTASLTITGAQAEADYVYCNRSRDSGNHVVFGGGTKLTVLAAA 263

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RESULT 12
US-10-029-988B-203
; Sequence 203, Application US/10029988B
; Publication No. US20040001839A1
/ GENERAL INFORMATION:
/ APPLICANT: Bio-Technology General Corp.
/ TITLE OF INVENTION: Y17-ISOLATED MOLECULES CONTAINING EPITOPES COMPRISING EPITOPES CONTAINING SULFATED
/ TITLE OF INVENTION: MOJETTES ANTIBODIES TO SUCH EPITOPES AND USE THEREOF

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/ FILE REFERENCE: 10793/46
/ CURRENT APPLICATION NUMBER: US/10/029,988B
/ CURRENT FILING DATE: 2001-12-31
/ PRIOR APPLICATION NUMBER: 60/258,948
/ PRIOR FILING DATE: 2000-12-29
/ NUMBER OF SEQ ID NOS: 204
/ SOFTWARE: FastSEQ for Windows Version 3.0
/ SEQ ID NO 203
/ LENGTH: 277
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-029-988B-203

```

Query Match	100.0%;	Score 576;	DB 15;	Length 277;
Best Local Similarity	100.0%;	Pred. NO. 8e-44;		

Qy 61 SGSSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGTTKLTVLGAAA 111
Db 213 SGSSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGTTKLTVLGAAA 263

RESULT 15

US-10-029-926B-25
; Sequence 25, Application US/10029926B
; Publication No. US20040073011A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/23/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-926B-25

Query Match 100.0%; Score 576; DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 8e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELTQDPAVSVALGQTVRITCQDLSLSYASWYQKPGQAPVLVIYKKNRPSGIPDRF 60
Db 153 SELTQDPAVSVALGQTVRITCQDLSLSYASWYQKPGQAPVLVIYKKNRPSGIPDRF 212

Qy 61 SGSSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGTTKLTVLGAAA 111
Db 213 SGSSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGTTKLTVLGAAA 263

Search completed: April 25, 2005, 21:09:46
Job time : 50.1009 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 18, 2005, 21:47:37 ; Search time 49.3722 Seconds
(without alignments)
939.375 Million cell updates/sec

Title: US-10-029-926d-7

Perfect score: 576

Sequence: 1 SELTQDPAVSVALGQTVRIT.....SGNHVFGGTKLTVLGAAA 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA_Main:

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:**

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:**

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:**

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:**

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:**

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	576	100.0	111	4	US-10-032-037B-7
2	576	100.0	111	4	US-10-029-988B-7
3	576	100.0	111	4	US-10-032-423A-7
4	576	100.0	111	4	US-10-029-926B-7
5	576	100.0	112	6	US-11-039-767-18
6	576	100.0	125	5	US-10-888-959-8
7	576	100.0	266	4	US-10-032-037B-204
8	576	100.0	266	4	US-10-029-988B-204
9	576	100.0	266	4	US-10-032-423A-204
10	576	100.0	277	4	US-10-032-037B-25
11	576	100.0	277	4	US-10-032-037B-203
12	576	100.0	277	4	US-10-029-988B-25
13	576	100.0	277	4	US-10-029-988B-203
14	576	100.0	277	4	US-10-032-423A-25
15	576	100.0	277	4	US-10-032-423A-203
16	576	100.0	277	4	US-10-029-926B-25
17	576	100.0	277	4	US-10-029-926B-203
18	576	100.0	277	4	US-10-610-843B-1
19	576	100.0	278	4	US-10-610-843B-2
20	576	100.0	280	4	US-10-610-843B-3
21	576	100.0	280	4	US-10-611-588C-1
22	576	100.0	280	5	US-10-880-922-5
23	576	100.0	280	5	US-10-880-922-6
24	576	100.0	280	5	US-10-880-922-55
25	576	100.0	280	5	US-10-880-922-56
26	576	100.0	280	5	US-10-880-922-60
27	576	100.0	280	5	US-10-880-922-61

28	576	100.0	309	4	US-10-052-798-9	Sequence 9, Appli
29	576	100.0	309	4	US-10-288-917-9	Sequence 9, Appli
30	576	100.0	309	4	US-10-423-448-9	Sequence 9, Appli
31	576	100.0	312	4	US-10-052-798-10	Sequence 10, Appli
32	576	100.0	312	4	US-10-288-917-10	Sequence 10, Appli
33	576	100.0	312	4	US-10-423-448-10	Sequence 10, Appli
34	568	98.6	110	4	US-10-800-197-115	Sequence 115, App
35	568	98.6	110	4	US-10-800-197-119	Sequence 119, App
36	564	97.9	153	3	US-09-988-115A-59	Sequence 59, Appli
37	564	97.9	153	5	US-10-705-519-59	Sequence 59, Appli
38	564	97.9	237	3	US-09-880-748-1941	Sequence 1941, Ap
39	564	97.9	237	3	US-09-880-748-2112	Sequence 2112, Ap
40	564	97.9	237	4	US-10-293-418-1941	Sequence 1941, Ap
41	564	97.9	237	4	US-10-293-418-2112	Sequence 2112, Ap
42	564	97.9	238	3	US-09-880-748-1907	Sequence 1907, Ap
43	564	97.9	238	4	US-10-293-418-1907	Sequence 1907, Ap
44	564	97.9	238	6	US-11-090-847-81	Sequence 81, Appli
45	564	97.9	238	6	US-11-090-847-103	Sequence 103, App

ALIGNMENTS

RESULT 1

US-10-032-037B-7

Sequence 7, Application US/10032037B

Publication No. US20040001822A1

GENERAL INFORMATION:

APPLICANT: Bio-Technology General Corp.

TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF

FILE REFERENCES: 10793/44

CURRENT APPLICATION NUMBER: US/10/032,037B

CURRENT FILING DATE: 2001-12-31

PRIOR APPLICATION NUMBER: 60/258,948

PRIOR FILING DATE: 2000-12-29

NUMBER OF SEQ ID NOS: 204

SOFTWARE: Fast-SEQ for Windows Version 3.0

SEQ ID NO 7

LENGTH: 111

TYPE: PRT

ORGANISM: Homo sapiens

US-10-032-037B-7

Query Match 100.0%; Score 576; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.1e-44;

Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELTQDPAVSVALGQTVRITCCGDSLSRSYASVYQKPGQAPVLVIYKNNRPSGIDPRF 60

Db 1 SELTQDPAVSVALGQTVRITCCGDSLSRSYASVYQKPGQAPVLVIYKNNRPSGIDPRF 60

Qy 61 SGSSSGNTASLTITGAQAEADYDCNSRDSGNHVVFGGTKLTVLGAAA 111

Db 61 SGSSSGNTASLTITGAQAEADYDCNSRDSGNHVVFGGTKLTVLGAAA 111

RESULT 2

US-10-029-988B-7

Sequence 7, Application US/10029988B

Publication No. US20040001839A1

GENERAL INFORMATION:

APPLICANT: Bio-Technology General Corp.

TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF

FILE REFERENCES: 10793/46

CURRENT APPLICATION NUMBER: US/10/029,988B

CURRENT FILING DATE: 2001-12-31

PRIOR APPLICATION NUMBER: 60/258,948

PRIOR FILING DATE: 2000-12-29

NUMBER OF SEQ ID NOS: 204

SOFTWARE: Fast-SEQ for Windows Version 3.0

SEQ ID NO 7

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; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-7

Query Match      100.0%; Score 576; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.1e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTQDPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLVIYGNRPSGIPDRF 60
   |||||||
Db 1 SELTQDPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLVIYGNRPSGIPDRF 60
   |||||||

QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGTKLTVLGAAA 111
   |||||||
Db 61 SGSSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGTKLTVLGAAA 111
   |||||||

RESULT 3
US-10-032-423A-7
; Sequence 7, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-7

Query Match      100.0%; Score 576; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.1e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTQDPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLVIYGNRPSGIPDRF 60
   |||||||
Db 1 SELTQDPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLVIYGNRPSGIPDRF 60
   |||||||

QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGTKLTVLGAAA 111
   |||||||
Db 61 SGSSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGTKLTVLGAAA 111
   |||||||

RESULT 4
US-10-029-926B-7
; Sequence 7, Application US/10029926B
; Publication No. US20040073011A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-926B-7

Query Match      100.0%; Score 576; DB 4; Length 111;
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Best Local Similarity 100.0%; Pred. No. 4.1e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTQDPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLVIYGNRPSGIPDRF 60
   |||||||
Db 1 SELTQDPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLVIYGNRPSGIPDRF 60
   |||||||

QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGTKLTVLGAAA 111
   |||||||
Db 61 SGSSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGTKLTVLGAAA 111
   |||||||

RESULT 5
US-11-039-767-18
; Sequence 18, Application US/11039767
; Publication No. US20050170398A1
; GENERAL INFORMATION:
; APPLICANT: CRUCCELL HOLLAND B.V.
; TITLE OF INVENTION: Recombinant production of mixtures of antibodies
; FILE REFERENCE: 0079 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/039,767
; CURRENT FILING DATE: 2005-01-18
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: common VL sequence of clones B28 (anti-CD22 phase), II-2
; OTHER INFORMATION: (anti-CD72 phase) and I-2 (anti-class II phage)
US-11-039-767-18

Query Match      100.0%; Score 576; DB 6; Length 112;
Best Local Similarity 100.0%; Pred. No. 4.1e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTQDPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLVIYGNRPSGIPDRF 60
   |||||||
Db 2 SELTQDPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLVIYGNRPSGIPDRF 61
   |||||||

QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGTKLTVLGAAA 111
   |||||||
Db 62 SGSSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGTKLTVLGAAA 112
   |||||||

RESULT 6
US-10-888-959-8
; Sequence 8, Application US/10888959
; Publication No. US20050048545A1
; GENERAL INFORMATION:
; APPLICANT: Cull, Millard
; APPLICANT: Brennan, Miles
; APPLICANT: Gill, Ronald
; TITLE OF INVENTION: Universal Detection of Binding
; FILE REFERENCE: BPP-03
; CURRENT APPLICATION NUMBER: US/10/888,959
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/487,018
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: US 60/509,196
; PRIOR FILING DATE: 2003-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: variable light chain domain
US-10-888-959-8

Query Match      100.0%; Score 576; DB 5; Length 125;
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Best Local Similarity 100.0%; Pred. No. 4.6e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELTQDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIYKNNRPSGIPDRF 60
|||||
Db 1 SELTQDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIYKNNRPSGIPDRF 60
|||||

Qy 61 SGSSSGNTASITITGAQAEDADYYCNSRDSGNHVVFGGKTLTVLGAAA 111
|||||
Db 61 SGSSSGNTASITITGAQAEDADYYCNSRDSGNHVVFGGKTLTVLGAAA 111
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RESULT 7

US-10-032-037B-204
; Sequence 204, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 204
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-204

Query Match 100.0%; Score 576; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 1e-43;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELTQDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIYKNNRPSGIPDRF 60
|||||
Db 153 SELTQDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIYKNNRPSGIPDRF 212
|||||

Qy 61 SGSSSGNTASITITGAQAEDADYYCNSRDSGNHVVFGGKTLTVLGAAA 111
|||||
Db 213 SGSSSGNTASITITGAQAEDADYYCNSRDSGNHVVFGGKTLTVLGAAA 263
|||||

RESULT 8

US-10-029-988B-204
; Sequence 204, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 204
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-204

Query Match 100.0%; Score 576; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 1e-43;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELTQDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIYKNNRPSGIPDRF 60
|||||

Db 153 SELTQDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIYKNNRPSGIPDRF 212
|||||
Qy 61 SGSSSGNTASITITGAQAEDADYYCNSRDSGNHVVFGGKTLTVLGAAA 111
|||||
Db 213 SGSSSGNTASITITGAQAEDADYYCNSRDSGNHVVFGGKTLTVLGAAA 263
|||||

RESULT 9

US-10-032-423A-204
; Sequence 204, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 204
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-204

Query Match 100.0%; Score 576; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 1e-43;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELTQDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIYKNNRPSGIPDRF 60
|||||
Db 153 SELTQDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIYKNNRPSGIPDRF 212
|||||

Qy 61 SGSSSGNTASITITGAQAEDADYYCNSRDSGNHVVFGGKTLTVLGAAA 111
|||||
Db 213 SGSSSGNTASITITGAQAEDADYYCNSRDSGNHVVFGGKTLTVLGAAA 263
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RESULT 10

US-10-032-037B-25
; Sequence 25, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-25

Query Match 100.0%; Score 576; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 1.1e-43;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELTQDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIYKNNRPSGIPDRF 60
|||||
Db 153 SELTQDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIYKNNRPSGIPDRF 212
|||||

Qy 61 SGSSSGNTASITITGAQAEDADYYCNSRDSGNHVVFGGKTLTVLGAAA 111
|||||
Db 213 SGSSSGNTASITITGAQAEDADYYCNSRDSGNHVVFGGKTLTVLGAAA 263
|||||

FILE REFERENCE: 10793/45
CURRENT APPLICATION NUMBER: US/10/032,423A
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: 60/258,948
PRIOR FILING DATE: 12/29/2000
NUMBER OF SEQ ID NOS: 204
SOFTWARE: PatSeq for Windows Version 3.0
SEQ ID NO 203
LENGTH: 277
TYPE: PRT
ORGANISM: Homo sapiens
US-10-032-423A-203

Query Match 100.0%; Score 576; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 1.1e-43;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SELTQDPAVSVALGQTVRITCGDSLRSYYASWYQKPGQAPVLVIYGNRPSGIPDRF 60
Db 153 SELTQDPAVSVALGQTVRITCGDSLRSYYASWYQKPGQAPVLVIYGNRPSGIPDRF 212
Qy 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGAAA 111
Db 213 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGAAA 263

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Job time : 50.3722 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2005, 21:53:49 ; Search time 1.40063 Seconds
(without alignments)
89.536 Million cell updates/sec

Title: US-10-029-926D-7

Perfect score: 5%

Sequence: 1 SELTQDPAPVVALGQTVRIT.....SGNHVFGGTKLTVLGAAA 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	298	51.7	258	1	US-10-512-184-26
2	298	51.7	327	1	US-10-512-184-62
3	298	51.7	327	1	US-10-512-184-64
4	298	51.7	328	1	US-10-512-184-63
5	298	51.7	575	1	US-10-512-184-65
6	298	51.7	625	1	US-10-512-184-47
7	297.5	51.6	252	1	US-10-512-184-28
8	292	50.7	261	1	US-10-512-184-35
9	292	50.7	313	1	US-10-512-184-72
10	286	49.7	250	1	US-10-512-184-27
11	254	44.1	106	7	US-11-174-186-7
12	250.5	43.5	128	1	US-10-721-763-31
13	249	43.2	626	1	US-10-512-184-49
14	248.5	43.1	259	1	US-10-512-184-34
15	248.5	43.1	371	1	US-10-512-184-71
16	247.5	43.0	543	1	US-10-495-664-3
17	246.5	42.8	131	1	US-10-721-763-27
18	244	42.4	106	7	US-11-174-186-11
19	244	42.4	106	7	US-11-174-186-12
20	244	42.4	106	7	US-11-174-186-13
21	243	42.2	106	7	US-11-174-186-15
22	242	42.0	106	7	US-11-174-186-10
23	242	42.0	106	7	US-11-174-186-14
24	241.5	41.9	263	1	US-10-512-184-29
25	239	41.5	106	7	US-11-174-186-1

26	239	41.5	106	7	US-11-174-186-9	Sequence 9, Appli
27	239	41.5	106	7	US-11-174-186-16	Sequence 12, Appl
28	239	41.5	213	7	US-11-174-186-42	Sequence 46, Appl
29	238.5	41.4	129	1	US-10-721-763-19	Sequence 19, Appl
30	238	41.3	113	1	US-10-932-334-61	Sequence 7, Appli
31	236	41.0	109	1	US-10-726-554-7	Sequence 61, Appli
32	235	40.8	127	1	US-10-839-799-27	Sequence 27, Appli
33	234	40.6	106	7	US-11-174-186-8	Sequence 8, Appli
34	233.5	40.5	259	1	US-10-512-184-31	Sequence 31, Appl
35	233.5	40.5	329	1	US-10-512-184-68	Sequence 68, Appl
36	232	40.3	113	1	US-10-932-334-64	Sequence 64, Appl
37	231.5	40.2	110	1	US-10-648-816-2	Sequence 2, Appli
38	231.5	40.2	110	1	US-10-648-816-3	Sequence 3, Appli
39	231.5	40.2	110	1	US-10-648-816-4	Sequence 4, Appli
40	231.5	40.2	110	1	US-10-648-816-5	Sequence 6, Appli
41	231.5	40.2	110	1	US-10-648-816-7	Sequence 7, Appli
42	231.5	40.2	110	1	US-10-648-816-8	Sequence 8, Appli
43	231.5	40.2	126	1	US-10-839-799-75	Sequence 75, Appli
44	231.5	40.2	129	1	US-10-721-763-23	Sequence 23, Appl
45	231	40.1	112	7	US-11-012-353-56	Sequence 56, Appl

ALIGNMENTS

RESULT 1

US-10-512-184-26
; Sequence 26, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512.184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 26
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv CWP2
; OTHER INFORMATION: with specificity against Fusarium spp.; originates
; OTHER INFORMATION: from Gallus gallus.
US-10-512-184-26

Query Match 51.7%; Score 298; DB 1; Length 258;
Best Local Similarity 59.5%; Pred No. 2.2e-16;
Matches 66; Conservative 10; Mismatches 27; Indels 8; Gaps 4;

Qy 3 LTQDPAPVVALGQTVRITCGDSLRSYASWYQOK-FQAPVLVIYGN---NRPSGIPD 58

Db 149 LTQPSVSANLGGTVEITCSG---GYRCWFQKSPGAPVTIYDDDSANRPSNIPS 205

Qy 59 RFGSSSGNTASLTITCAQAEADYDCNSRDSSGNHV-VFGGTKLTVLG 108

Db 206 RFGSGTSGTATLTITGVQADDEAVYFCGSDYDRSSGYVSIFGAGTTTLTVLG 256

RESULT 2

US-10-512-184-62
; Sequence 62, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512.184

FILE REFERENCE: 3581.01US01
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 47
LENGTH: 625
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: fusion protein
OTHER INFORMATION: comprising the leader peptide - chitinase - linker
OTHER INFORMATION: - scFv CWP2 - cmcy/His6.
US-10-512-184-47

Query Match 51.7%; Score 298; DB 1; Length 625;
Best Local Similarity 59.5%; Pred. No. 4.5e-16;
Matches 66; Conservative 10; Mismatches 27; Indels 8; Gaps 4;
QY 3 LTQDPVSVVALGQTVRTITCGDLSLSYASWYQOK-PQAPVLVIYGNK---NRPSGIPD 58
DB 490 LTQPSVSVANLGTVEITCSGG--GYRYGWFQKSPGAPVTVIYWDSDSANRPSNIPS 546
QY 59 RFGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHV-VFGGQTKLTVLG 108
DB 547 RFGSGTSGTATLTITGVQADDEAVYFCGYSYDRSGYVIFGAGTTLTVLG 597

RESULT 7

US-10-512-184-28
Sequence 28, Application US/10512184
Publication No. US20050244901A1
GENERAL INFORMATION:
APPLICANT: Fraunhofer Gesellschaft zur Forderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: resistance against fungi
FILE REFERENCE: 3581.01US01
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
LENGTH: 252
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: scFv FPCWPA5
OTHER INFORMATION: with specificity against Fusarium spp.; originates
OTHER INFORMATION: from Gallus gallus.
US-10-512-184-28

Query Match 51.6%; Score 297.5; DB 1; Length 252;
Best Local Similarity 59.8%; Pred. No. 2.4e-16;
Matches 64; Conservative 10; Mismatches 28; Indels 5; Gaps 4;
QY 3 LTQDPVSVVALGQTVRTITCGDLSLSYASWYQOK-PQAPVLVIYGNKRPSPGIPDRFS 61
DB 148 LTQPSVSVANLGTVEITCSGG--GSY--GWYQKSPGAPVTVIYSDNRPSNIPS 204
QY 62 GSSSGNTASLTITGAQAEDEADYYCNSRDSGNHV-VFGGQTKLTVLG 108
DB 205 GSKSGSANTLTITGVQVEDEAVYCGSADSNNTN-AIFGAGTTLTVLG 250

RESULT 8

US-10-512-184-35
Sequence 35, Application US/10512184
Publication No. US20050244901A1
GENERAL INFORMATION:
APPLICANT: Fraunhofer Gesellschaft zur Forderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease

TITLE OF INVENTION: resistance against fungi
FILE REFERENCE: 3581.01US01
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 35
LENGTH: 261
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: scFv PLp9 with
OTHER INFORMATION: specificity against Phoma lingam; originates from
OTHER INFORMATION: Mus musculus.
US-10-512-184-35

Query Match 50.7%; Score 292; DB 1; Length 261;
Best Local Similarity 57.3%; Pred. No. 6.1e-16;
Matches 63; Conservative 12; Mismatches 29; Indels 6; Gaps 4;
QY 3 LTQDPVSVVALGQTVRTITCGDLSLSYASWYQOK-PQAPVLVIYGNKRPSPGIPDR 59
DB 152 LTQASSVSANLGTVEITCSGGSYAGSYGYQKTPGSAFVTVIYSDNRPSNIPS 211
QY 60 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHV-VFGGQTKLTVLG 108
DB 212 FSGSLSGSTNTLTITGVQVDEAVYFCGAYDN--NYAGIFGAGTTLTVLG 259

RESULT 9

US-10-512-184-72
Sequence 72, Application US/10512184
Publication No. US20050244901A1
GENERAL INFORMATION:
APPLICANT: Fraunhofer Gesellschaft zur Forderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: resistance against fungi
FILE REFERENCE: 3581.01US01
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 72
LENGTH: 313
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: precursor
OTHER INFORMATION: fusion protein comprising MBP - linker -
OTHER INFORMATION: scFv PLp9.
US-10-512-184-72

Query Match 50.7%; Score 292; DB 1; Length 313;
Best Local Similarity 57.3%; Pred. No. 7.1e-16;
Matches 63; Conservative 12; Mismatches 29; Indels 6; Gaps 4;
QY 3 LTQDPVSVVALGQTVRTITCGDLSLSYASWYQOK-PQAPVLVIYGNKRPSPGIPDR 59
DB 204 LTQASSVSANLGTVEITCSGGSYAGSYGYQKTPGSAFVTVIYSDNRPSNIPS 263
QY 60 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHV-VFGGQTKLTVLG 108
DB 264 FSGSLSGSTNTLTITGVQVDEAVYFCGAYDN--NYAGIFGAGTTLTVLG 311

RESULT 10

US-10-512-184-27
Sequence 27, Application US/10512184
Publication No. US20050244901A1
GENERAL INFORMATION:
APPLICANT: Fraunhofer Gesellschaft zur Forderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease

; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv PL2 with
; OTHER INFORMATION: specificity against Phoma lingam; originates from
; OTHER INFORMATION: Mus musculus.
US-10-512-184-34

Query Match 43.1%; Score 248.5; DB 1; Length 259;
Best Local Similarity 45.9%; Pred. No. 8.1e-13;
Matches 51; Conservative 21; Mismatches 30; Indels 9; Gaps 3;
Qy 3 LTQDP-AVSVALGQTVRITCO-----GDSLSRYASWYQKPGQAPVLVIYGNRPSPG 55
Db 148 LTQSPSSLMSVGGKVTMSCKSSQSLNSSNKNYLAWYQKPGQSPKLLVYPASTRESG 207
Qy 56 IPDRFGSSSGNTASLTITGAQDEADYDCNSRDSSGNHVHVFGGTKLTV 106
Db 208 VPDRFIGSGGTDFTLTITSSVQABDLADYFCQGHYST--PPTFGGKLEI 256

RESULT 15

US-10-512-184-71
; Sequence 71, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: precursor
; OTHER INFORMATION: fusion protein comprising ACE - linker -
; OTHER INFORMATION: scFv PL2.
US-10-512-184-71

Query Match 43.1%; Score 248.5; DB 1; Length 371;
Best Local Similarity 45.9%; Pred. No. 1.1e-12;
Matches 51; Conservative 21; Mismatches 30; Indels 9; Gaps 3;
Qy 3 LTQDP-AVSVALGQTVRITCO-----GDSLSRYASWYQKPGQAPVLVIYGNRPSPG 55
Db 260 LTQSPSSLMSVGGKVTMSCKSSQSLNSSNKNYLAWYQKPGQSPKLLVYPASTRESG 319
Qy 56 IPDRFGSSSGNTASLTITGAQDEADYDCNSRDSSGNHVHVFGGTKLTV 106
Db 320 VPDRFIGSGGTDFTLTITSSVQABDLADYFCQGHYST--PPTFGGKLEI 368

Search completed: November 18, 2005, 22:18:06
Job time : 2.40063 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2005, 21:35:01 ; Search time 10.8549 Seconds
(without alignments)
983.894 Million cell updates/sec

Title: US-10-029-926D-7

Perfect score: 576

Sequence: 1 SEITQDPAVSVALGQTVIRIT.....SGNHVRFGGTKLTVLGAAA 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	564	97.9	109	2 S19663	Ig lambda chain V-
2	558	96.9	108	2 S47184	Ig lambda chain V
3	547.5	95.1	110	2 S36272	Ig lambda chain V
4	542	94.1	127	2 S70444	Ig lambda chain pr
5	541	93.9	108	2 S38498	Ig lambda chain -
6	535	92.9	109	2 S38496	Ig lambda chain -
7	527	91.5	108	1 L3HUSH	Ig lambda chain V-
8	526	91.3	233	2 S25748	Ig lambda chain -
9	517.5	89.8	146	2 S02083	Ig lambda chain V-
10	514.5	89.3	110	2 S19672	Ig lambda chain V
11	499	86.6	96	2 S36060	Ig lambda chain -
12	498	86.6	115	2 S13726	Ig lambda chain V
13	498	86.5	233	2 S25741	Ig lambda chain -
14	438.5	76.1	106	2 S38495	Ig lambda chain -
15	420	72.9	105	2 S49535	anti-Sm antibody V
16	414	71.9	190	2 S25740	Ig lambda chain V
17	410	71.2	119	2 S30526	Ig lambda chain -
18	397	68.9	107	2 PC4283	anti-SS-A/Ro 60K p
19	395.5	68.7	120	2 S30525	Ig lambda chain V
20	384	66.7	226	2 S25745	Ig lambda chain -
21	381	66.1	231	2 S25751	Ig lambda chain -
22	381	66.1	231	2 S25738	Ig lambda chain -
23	376	65.3	120	2 S30527	Ig lambda chain V
24	376	65.3	151	2 S25739	Ig lambda chain -
25	376	65.3	231	2 S25753	Ig lambda chain -
26	374	64.9	233	2 S25747	Ig lambda chain -
27	373.5	64.8	212	2 S70431	Ig lambda chain -
28	370	64.2	107	1 L4HURL	Ig lambda chain V-
29	370	64.2	108	1 L5HUDL	Ig lambda chain V-

ALIGNMENTS

RESULT 1

S19663

Ig lambda chain V region (clone alpha-BSA3) - human

C;Species: Homo sapiens (man)

C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000

C;Accession: S19663

R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991

A;Title: BY-passing immunization. Human antibodies from V-gene libraries displayed on ph

A;Reference number: S19663; MUID:92085276; PMID:1748994

A;Accession: S19663

A;Molecule type: mRNA

A;Residues: 1-109 <MAR>

A;Cross-references: UNIPARC:UPI0000039C3B; EMBL:X61640; NID:929492; PIDN:CAA43821.1; PID

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

P;15-89/Domain: immunoglobulin homology <IMM>

Query Match 97.9%; Score 564; DB 2; Length 109;

Best Local Similarity 100.0%; Pred. No. 1.7e-41;

Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEITQDPAVSVALGQTVIRITCGDLSRSYASVYQKPGQAPVLVIYKGNRPSGIPDRF 60

Db 2 SEITQDPAVSVALGQTVIRITCGDLSRSYASVYQKPGQAPVLVIYKGNRPSGIPDRF 61

Qy 61 SGSSSGNTASLTITGAQAEADYYCNSRDSGSHVYVFGGTKLTVLG 108

Db 62 SGSSSGNTASLTITGAQAEADYYCNSRDSGSHVYVFGGTKLTVLG 109

RESULT 2

S47184

Ig lambda chain - human

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

R;McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.

submitted to the EMBL Data Library, June 1994

A;Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patient

A;Reference number: S47184

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-108 <MCI>

A;Cross-references: UNIPARC:UPI0000031AF6; EMBL:X79783; NID:9506426; PIDN:CAA56179.1; PI

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

P;15-89/Domain: immunoglobulin homology <IMM>

Query Match 96.9%; Score 558; DB 2; Length 108;

Best Local Similarity 100.0%; Pred. No. 5.3e-41;

	Matches	107;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	SEITQDPAVSAVGQTVRIITCGDSLSRYASWYQQKPGQAPVLIIVGKNNRPSGIDPRF	60							
Db	2	SEITQDPAVSAVGQTVRIITCGDSLSRYASWYQQKPGQAPVLIIVGKNNRPSGIDPRF	61							
Qy	61	SGSSSGNTASLTITGAQAEADYYICNSRDSSGNNHVVFGGCKLTVL	107							
Db	62	SGSSSGNTASLTITGAQAEADYYICNSRDSSGNNHVVFGGCKLTVL	108							

RESULT 3

S36272
IG lambda chain V region (clone alpha-THY-29) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C/Accession: S36272
R/Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A/Title: Human anti-self antibodies with high specificity from phage display libraries.
A/Reference number: S36256; MUID:93178448; PMID:7679990
A/Accession: S36272
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-110 <GRI>
A/Cross-references: UNIPARC:UPI0000118DF6; EMBL:Z18833; NID:g33419; PIDN:CAA79285.1; PID
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-89/Domain: immunoglobulin homology <IMM>

RESULT 4

S70444

Ig lambda chain precursor V region - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 31-Dec-2004

C:Accession: S70444, S70426

R:Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.

Mol. Immunol. 29, 1363-1373, 1992

A>Title: IGM kappa/lambda BBV human B cell clone: an early step of differentiation of f

A:Reference number: S70442; MUID:93024508; PMID:1383695

A:Accession: S70444

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-127 <CUI>

A:Cross-references: UNIPROT:Q9NSD6; UNIPARC:UPI0000176807

A:Experimental source: clone E29.1

R:Tonnelle, C.

submitted to the EMBL Data Library, May 1990

A:Reference number: S70426

A:Accession: S70426

A:Molecule type: mRNA

A:Residues: 1-90 <TON>

A:Cross-references: UNIPARC:UPI0000176808; EMBL:X53070

A:Experimental source: cell line E29.1, clone VL 29-1

C:Superfamily: immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-127/Product: Ig lambda chain V region (fragment) #status predicted <MAT>

F:34-108/Domain: immunoglobulin homology <IMW>

	Query Match	94.1%	Score 542;	DB 2;	Length 127;
	Best Local Similarity	97.2%	Pred. No. 1.5e-39;		
	Matches 104;	Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	1	SELTQDPAVSVALGQTVRITCQDLSRSYASWYQKPGQAPLVLYGKNNRPSGIDPRF	60		
Db	21	SELTQDPAVSVALGQTVRITCQDLSRSYASWYQKPGQAPLVLYGKNNRPSGIDPRF	80		
Qy	61	SGSSSGNTASLTITGCAEADYDNCNRDSSGNHVVFEGGTKLTVL	107		
Db	81	SGSSSGNTASLTITGCAEADYDNCNRDSSGNHVVFEGGTKLTVL	127		

RESULT 5

S38498
Ig lambda chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C/Accession: S38498
R/Marks, J.D.; Ouweland, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Thorpe, S
submitted to the EMBL Data Library, June 1993
A/Description: Human antibody fragments specific for human blood group antigens from a ph
A/Reference number: S38488
A/Accession: S38498
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-108 <MAR>
A/Cross-references: UNIPARC:UPI000011654E; EMBL:Z23035; NID:G414043; PIDN:CAA80570.1; P
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:14-88/Domain: immunoglobulin homology <IMM>

RESISTANCE

```

Accession 6
S38496
Ig lambda chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S38496
R:Marks, J.D.; Ouehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S
A:Submitted to the EMBL Data Library, June 1993
A:Description: Human antibody fragments specific for human blood group antigens from a p
A:Reference number: S38488
A:Accession: S38496
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-109 <MAP>
A:Cross-references: UNIPARC:UPI000011654A; EMBL:Z23031; NID:g414039; PIDN:CAA80566.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-89/Domain: immunoglobulin homology <IMM>

Query Match          92.9%; Score 535; DB 2; Length 109;
Best Local Similarity 93.5%; Pred. No. 5e-39;
Matches 101; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SELTQDPAVSVALGQTVRITCGDLSRYSYASWYQKPGQAPVLVIYKKNRPSPGIDPRF 60
Db 2 SELTQDPAVSVALGQTVRITCGDLSKYSYASWYQKPGQAPVLVMYKKNRPSPGIDPR 61
Ov 61 SGSSSGNTASLTITGAQAEADRDYYCNSRDSNGHVVFVGGGTKLTVLG 108

```

Qy	1	SELTQDPAVSVALGQTVTRITCOGDSLSRYASYQOKPGQAPVLVITVYGNRRPSGIPDRP	60
Db	21	SELTQDPAVSVALGQTVTRITCOGDSLSRYASYQOKPGQAPVLVITVYGNRRPSGIPDRP	80
Qy	61	SGSSSGNTASLTITGAQAEADYVYCNRSRDSGNHVVFQGGTKLTVLG	108
Db	81	SGSSSGNTASFTATGAQAEADYVYCNRSRDSGDOVLFGGTKLTVLG	28

S36060
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C;Accession: S36060
R;Williams, S.C.
submitted to the EMBL Data Library, April 1993

Qy 64 SSGNTASLITITGAQAEDEADYYCNSRDSGNNHVVFGGKLTVLG 108
| | | : | | | | | | | | | | : | | | | | | | | | |
Db 61 SSGTTLTITISGVQAEDEADYYCQADSSGTYVVVFGGKLTVLG 105
| | | : | | | | | | | | | | : | | | | | | | | | |

Search completed: November 18, 2005, 21:47:21
Job time : 11.8549 secs

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RESULT 2

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LV3A_HUMAN
ID LV3A_HUMAN STANDARD; PRT; 108 AA.
AC P01714;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE IG lambda chain V-III region SH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=70156723; PubMed=4909564;
RA Titani K., Wikier M., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a lambda type Bence-Jones protein. 3. The
RT complete amino acid sequence and the location of the disulfide
RT bridges."
RL J. Biol. Chem. 245:2171-2176 (1970).
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; A01980; L3HUSH.
DR HSP; P01703; 7PAB.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv_1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 97 Ig-like.
FT DISULFID 21 86
FT NON TER 108 108
FT SEQUENCE 108 AA; 11393 MW; E7E1229586411A56 CRC64;
Query Match 91.5%; Score 527; DB 1; Length 108;
Best Local Similarity 92.6%; Pred. No. 3e-44;
Matches 100; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
QY 1 SELTQDPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLVIYGNRNPSPGIPDRF 60
Db 1 SELTQDPAVSVALGQTVRITCGDLSRGLGYDAWYQKPGQAPLLVIYGRNRPSPGIPDRF 60
QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGTTKLTVLG 108
Db 61 SGSSSGHTASLTITGAQAEADYYCNSRDSGKHVLFGGTTKLTVLG 108
RESULT 3
ID Q6GMW4_HUMAN PRELIMINARY; PRT; 233 AA.
AC Q6GMW4;
DT 03-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.

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TISSUE=Primary B-Cells;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE
TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073786; AAH73786.1; -; mRNA.
DR SNR; O6GMW4; 23-229.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG-LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 233 AA; 24855 MW; 462677B3B8FDE5BD CRC64;
Query Match 91.3%; Score 526; DB 2; Length 233;
Best Local Similarity 91.7%; Pred. No. 9.1e-44;
Matches 99; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
QY 1 SELTQDPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLVIYGNRNPSPGIPDRF 60
Db 21 SELTQDPAVSVALGQTVRITCGDLSRTYASWYQKPGQAPVLVIYAKDNRPSPGIPDRF 80
QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGTTKLTVLG 108
Db 81 SGSSSGHTASLTITGAQAEADYYCNSRDSGSHLVFGTGTKLTVLG 128
RESULT 4
ID Q5NV73_HUMAN PRELIMINARY; PRT; 97 AA.
AC Q5NV73;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE V2-13 protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]

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QY 19 ITCCGSLRSYASWTQKPGQAPVLVIYKNNRPSGIPDRFSGSSSGNTASLTITGAQA 78
Db 1 ITCCGSLRSYASWTQKPGQAPVLVIYKNNRPSGIPDRFSGSSSGNTASLTITGAQA 60
QY 79 EDEADYCNRSRDSGNHNVFG 99
Db 61 EDEADYCNRSRDSGNHNVFG 81

RESULT 7
ID Q8NSF4_HUMAN PRELIMINARY; PRT; 233 AA.
AC Q8NSF4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGLC1 protein.
GN Name=IGLC1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.W.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RG NIH MGC Project;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=3122211;
RZ Darivach P., Lefranc G., Lefranc M.P.;
RT "Human immunoglobulin C lambda 6 gene encodes the Kern-Oz-lambda chain
RT and C lambda 4 and C lambda 5 are pseudogenes."
RL Proc. Natl. Acad. Sci. U.S.A. 84:9074-9078(1987).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=90324891; PubMed=2115572; DOI=10.1084/jem.172.2.609;
RA Vasicek T.J., Leder P.;
RT "Structure and expression of the human immunoglobulin lambda genes."
RL J. Exp. Med. 172:609-620(1990).
DR EMBL; BC032452; AAH32452.1; -; mRNA.
DR PIR; A39949; A39949.
DR PIR; S12441; S12441.
DR PIR; S12443; S12443.
DR HSSP; P01842; I1L1.
DR SNR; Q8NSF4; 20-229.
DR Ensembl; ENSG00000100208; Homo sapiens.
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DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Immunoglobulin domain.
SQ SEQUENCE 233 AA; 24961 MW; F092CFB6AA6E3A9A CRC64;

Query Match 72.2%; Score 416; DB 2; Length 233;
Best Local Similarity 74.8%; Pred. No. 6.9e-33;
Matches 80; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

QY 2 ELTQDPVAVSVALGQTVIRITCGDSLRSYASWTQKPGQAPVLVIYKNNRPSGIPDRFS 61
Db 22 ELTQDPVSVSPQQTARITCSGDALPKYAYWYQKSGQTPVLVIYDDTERPSGIPDRFS 81
QY 62 GSSSGNTASLTITGAQAEADYCNRSRDSGNHNVFGGTTKLTVLG 108
Db 82 GSSSGTVAATLTLSGAQVEADYCYVSSDSGNHNVFGGTTKLTVLG 128

RESULT 8
Q8FWF9_HUMAN PRELIMINARY; PRT; 232 AA.
ID Q8FWF9;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.W.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RG Director MGC Project;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC089414; AAH89414.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.v.
DR Pfam; PF07654; C1-set; 1.
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DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 232 AA; 24795 MW; F74218EFCFBCAC1 CRC64;

Query Match 66.4%; Score 382.5; DB 2; Length 232;
Best Local Similarity 71.0%; Pred. No. 1.4e-29;
Matches 76; Conservative 10; Mismatches 20; Indels 1; Gaps 1;

Qy 2 ELTQDPVSVVAGQTVRTTCOGDSLSRYASWYQKPGQAPVLVIYGNRPSGIPDRFS 61
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 22 DLTQPPSVSVSPGQTARITCGDALPRKYAPWYQKSGQAPVLVIYDSKPSGIPDRFS 81
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Qy 62 GSSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGGTKLVLG 108
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 82 GSSSGTWTATLTISGAQVEDEGYCYSTDISG-YPVFGGTKVTVLG 127
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RESULT 9
Q8N355_HUMAN PRELIMINARY; PRT; 234 AA.
ID Q8N355_HUMAN STANDARD; PRT; 111 AA.
AC P80749;
DT 15-JUN-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE IG lambda chain V-III region LOI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Pahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RG NIH MGC Project;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
[3]
RN NUCLEOTIDE SEQUENCE.
RX PubMed=2111699;
RA Hughes-Jones N.C., Bye J.M., Beale D., Coadwell J.;
RT "Nucleotide sequences and three-dimensional modelling of the VH and VL
RT domains of two human monoclonal antibodies specific for the D antigen
RT of the human Rh-blood-group system.";
RL Biochem. J. 268:135-140 (1990).
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RN [1]
RP NUCLEOTIDE SEQUENCE
RX MEDLINE=9728902; PubMed=9074928;
RA Kawasaki K., Minoshima S., Nakato E., Shibuya K., Shintani A.,
RA Schmeits J.L., Wang J., Shimizu N.;
RT "One-negabase sequence analysis of the human immunoglobulin lambda
RT gene locus.";
RL Genome Res. 7:250-261(1997).
DR EMBL; D88994; BAA20890.1; -; Genomic_DNA.
DR SMR; Q5NV90; 1-92.
DR HGNC; HGNC:5908; IGLV3-25.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 97
SQ SEQUENCE 97 AA; 10405 MW; 224CA886FF48A991 CRC64;

Query Match 63.2%; Score 364; DB 2; Length 97;
Best Local Similarity 73.4%; Pred. No. 3.5e-28;
Matches 69; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 2 ELTQDPAVSVLGGTVRITCGDSLRSYASWYQKPGQAPVLVIYGNRPSPGIPDRFS 61
Db |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
3 ELTQPPSVSVSPGQTARITCGDALKQAYWYQKPGQAPVLVIYKDSRPSGIPERFS 62
QY 62 GS8SGNTASLTITGAQAEDADYYCNSRDSGNH 95
Db |||||:||||:|||||:|||||:|||||:|||||:|||||:
63 GS8SGTITVLTISGVQAEDADYYCQSDSSGTY 96

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